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Listing first 45 summaries
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A1454704 UI-R-BT0-
BG187880 RS76883 A
AW529324 UI-R-BT1-
AW159035 Za50e05.x
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BF348620 602019924
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## ALIGNMENTS

Source	FEATURES		COMMENT	TITLE	REFERENCE	ORGANISM	SOURCE	ACCESSION VERSION	RESULT 1 BG819678 LOCUS DEFINITION
	Plate: 11.AMJ0862 row: o column: 17 High quality sequence stop: 648. Location/Qualifiers	Tissue Procurement: David N. Louis, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	Contact: Robert Strausberg, Ph.D. Email: cqapbs-r@mail.nih.gov	National Institutes of Health, Mammalian Gene Collection (MGC)	1 (bases 1 to 653) NIH-MCC http://mdc.nci.nih.gov/.	Homo sapiens Fukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.	human.	BG819678 BG819678.1 G1:J4167265	BG819678 653 bp mRNA EST 22-MAY-2001 602783172F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4934248 5', mRNA sequence.

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Sus scrofa
Eukaryota; l
Generation and sequence characterization
         Caetano, A.R., Johnson, R.K. and Pomp, D
                         Mammalia;
                ukaryota; Metazoa;
ammalia; Eutheria;
(bases 1 to 499)
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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98.3%;
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Cetartiodactyla; Suina; Suidae;
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Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
Oligo-dT track not found, Not
is likely internal to the mes
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Contact: Pomp, D
Department of Animal Science
University of Nebraska, Linco
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/dev_staye="ADULT"
/lab_hos1-"DH10H (Life Technologies)"
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/strain∴"University of Nebraska,
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EST.
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cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1788947
Seq primer: M13 Forward.
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program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
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Bonaldo, M.F., Lenno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host-"DH10B (Lite Technologies)"
/lab_host-"DH10B (Lite Technologies)"
/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified
/note-"Vector: pT7T3D-Pac (Pharmacia) with a library
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(U1-R-BT0) consists of a mixture of individually tagged
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normalized libraries constructed from rat hipoccampus,
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="U1-K-BTO-qk-h-03-0-U1"
/clone=lib="U1-K-BTO"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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/clone_lib-"Selected chromosome 21 cDNA library"
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A1454704 A154704.1 GI:4295587
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Norway rat.
Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is ikely internal to the message. cDNA Library Preparation: M.
is ikely internal to the message. cDNA Library Preparation: M.
fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics (www.resqen.com) This clone is also
available Lhrough the I.M.A.G.E. Consortium at LLNL.
(info@inage.lln1.gov). JMAGE ID-1788947
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              //wete-"wector: pT/T3D-Pac (1 armacia) with a modified /note-"wector: pT/T3D-Pac (1 armacia) with a modified /note-"wector: pT/T3D-Pac (1 armacia) with a library polylinker; Site_1: Not I; Site_2: Eco RI; This library polylinker; Site_1: Not I; Site_2: Eco RI; This library (UI-K-BFO) consists of a mixture of individually Lagged (UI-K-BFO) consists of a mixture of individually Lagged normalized libraries constructed from rat hippocampus, liblalmus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. The Lag used to identify the source cortex and testis. The Lag used to identify the source lissue is a string of 3-6 nucleotides present between the clisue is a string of the library of origin of a clone within identification of the library of origin of a clone within the mixture. This library was then subtracted using a driver consisting of a mixture of all clones from UI-K-AO, UI-K-CP, UI-K-ED, UI-K-ED, UI-K-CO, UI-K-CI, UI-K-C2 and UI-K-C2P."
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/lab_host-"DH10B (Life Techn logies)"
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/clone_lib="UI-R-BT0"
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/db_xref-"taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                       BG187880 487 bp mRNA EST
RST6883 Athersys KAGE Library Homo sapiens cDNA,
BG187880
BG187880.1 G1:13/0056,
                                                                                                                                                                       Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001) in press
Contact: Scott J. Cain
                                                                                                                                                                                                                                           Harrington,J.J., Shert,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Dahl,T., Thornton,M., Kamachandran,R., Whittington,J., Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E., Veloso,N., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J.
                                                                                                                                                                                                                                                                                                    Eukaryola: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 487)
                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                Creation of Genome wide Protein Expression Libraries
                                                                                                                Athersys, inc.
3201 Carnega Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                 and Ducar, M.
                                                                                                                                                                                                                                                                                                                                                Homo suptens
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                                                                                     High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                     scain@athersys.com
uality sequence stop: 487
Location/Qualifiers
/organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone_lib-"Athersys RAGE Library"
/cell_line-"HT1080"
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pred. No. 3.6e-85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW529324 410 bp mRNA EST UI-R-BT1-akm-f-08-0-UI.S1 UI-R-BT1 Rattus norvegicus UI-R-BT1-akm-f-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                      Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa 7e1: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                            Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW529324
AW529324.1 GI:7171738
EST.
                                                                                                                                        Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurogna, i; Muridae; Murinae;
                                                                                                                                                                                                                                                                                   Contact:
                                                                                                                                                                                                                                                                                                                                  discovery
                                                                                                                                                                                                                                                                                                                                                 Normalization and subtraction: two
                                                                                                          Research Genetics (www.resgen.com)
Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                 Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BT1-akm-f-08-0-U1"
                                                /organism="Rattus norvegicus
                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 2.1e-68;
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                                                                                                                                                                                                                                                      AUTHORS
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hes 297; Conserv
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ca50e05.x1 Xenopus E
5', mkNA sequence.
AW159045
AW159045 GI:62710
Unpublished (1999)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
                                                                                                                                                                                                                Amphiria, ...
Xenopodinae; Xenopus.
1 (bases 1 to 427)
Schutz,K., de la Bastide,M., Hu
                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                    Expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                      Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                        African clawed frog
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/lab_host="DHIOB (Life Technologies)"
/lock="Vector: pT7T3D-Pac (Pharmacia) with a modified // note="Vector: pT7T3D-Pac (Pharmacia) with a modified // polylinker; Site_1: Not I; Site_2: Eco RI; The library polylinker; Site_1: Not I; Site_2: Eco RI; The library from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulia, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at ratest, eng. down. The subtraction has been previously in the site of the library from which this country is the site of the library from which this country is the site of the library from which this country is the site of the library from which this country is the site of the library from which this country is the site of the library from which this country is the site of the library from which this country is the site of the library from which this country is the site of the library from which this country is the library from which the library from which this country is the library from which library fro
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TAG_LI: UI-R-BT1
TAG_TI::UE-corpus-striatum
TAG_SEQ+CTAGG"
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/dev_stage="adult"
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EST library
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Pred. No. 3.3
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                                                                                                                                                                                                                         Huang, E.N., Na
., Spiegel, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mccombie@cshl.org
Plate: Za50 row: e column: 05
Plate: Za50 row: e column: 05
Seq primer: M13 universal forward primer
High quality sequence stop: 427.
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                                     Danio rerio
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Rasborinae; C
                                                                                                                                                                            BC307959 483 bp mRNA EST 22-FEB-7001 fm55b04.yl Zebrafish adult retina cDN \ Danio rerio cDNA cone 4199358 5' similar to TR:060469 060469 DOWN SYNDROME CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
        Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
                                                                                                                   EST
                                                                                                                                               MOLECULE. ;, mRNA sequence BG307959
                                                                                                                                    BC307959.1
                                                                                                     zebrafish
                      (bases 1 to 483)
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Hillier, L., Kucaba, T., Martin, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: Lambda Zap I; Site_1: XbaI; This library was supplied by Holly Cline (Cold Spring Harbor Labs). cDNA synthesis with oligo dT Xba I (Xba I cloning site). RNA: stage 50-56 tadpoles, total brain tissue, GTC extraction method."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Xenopus EST library"
/Lissue_type="total brain tissue"
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/db_xref="taxon:8355"
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79.8%;
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Enteleostei;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
Contact: Stephen L. Johnson
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
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WashU Zebrafish EST Project 1998
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Library constructed by: Susan E. Brockerhoff DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www.rzpd.de)
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/dev_stage-"1-2 years"
/lab_host*"E.Coli XL1-Blue MRF')"
/note="Vector: Lambda ZAP II (pBluescript SK-); Site_
Rocarl; Site_2: Sall; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number: 760"
a 130 c 114 g 107 t
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/clone="4199358"
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/strain-"wild-type"
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Pred. No. 1.1e-60;
0; Mismatches 127;
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602019924F1 NCI_CGAP_Brn67 Hc
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Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BF348620
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High quality sequence stop: 697.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 744)
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Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       ō:
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Salt; Cloned unidirectionally, Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCL_CGAP Library."
196 c 210 g 150 t
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/clone_lib="NCI_CGAP_Brn67"
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/db_xref="taxon:9606"
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99.3%;
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Pred. No. 2.2e-60;
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Best Local Similarity
Matches 277; Conserv
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                                                                                                                                                             ggccaatccctgggagccttggggtgaccattgaccatattgacttcacgagctccttga 1963
                                                                                                                                           GGCCAATCCCTGGGAGCC-TGGGGTGACCATTGACAATATTGACTTCACGAGCTCCTTGA
               ccyccyct4tygaycaccaaayccagttgattgtcagagt 2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AST-T29E0017 Genetrap T47D Human Breast Carcinoma sapiens genomic 5', DNA sequence.
CCGCCGCTGTGGAGCACCAAAGCCAGTTGATTGTCAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: henkelg@aurorabio.com

Pools of cells were isolated from a GenomeScreen(TM) library. The

Pools of cells were isolated by retroviral integration of a gene

library of cells was generated by retroviral integration of a gene

tagging element consisting of: 1) A promoterless beta-lactamase

proceeded by a splice acceptor as a reporter for gene expression;

2) A promoter driving neomycin resistance followed by a splice

denor to trap downstream exons. 3' RACE from neomycin gene was

denor to trap downstream exons. 3' RACE from neomycin gene was

portformed using total RNA from isolated pools. Output was shotgun

clared in pamp-1 and used to transform DH5-alpha competent

clared in pamp-1 and used to transform conservations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Greg Henkel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
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, Durick,K. and Pollok,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 8584046719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 8584048436
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Entheria; Primates; Catarrhini; Hominidae;
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/cell_type-"Epithelial"
/cell_line "T470"
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/db_xref-"taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Huroka, T., Hori, F., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., 1shii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Najaki, A., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinaqawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tayami, M., Tagawa, A., Takahashi, F., Sogabe, Y., Suzuki, H., Tayami, M., Tagawa, A., Takahashi, F., Sano, H., Tayami, M., Tayami, A., Yasunishi, A
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High-cificiency full-length cDNA cluning
Methods in enzymology. 303, 19-44 (1999)
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                                                                                                                                                                                                         Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-ros@qsc.riken.go.jp, URI:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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    cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Genomic Sciences Center and Genome
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/translation-"MCHTSGTCMPTGLCSSSLSPPPPSIALSTTMTISALQRTQPARS
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Hanagaki, T., Hara, A., Hayatsu, N., Hi amoto, K., Hiraoka, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Izaw, M., Kato, H., Ka, ai, J.,
Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H.,
Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yammura, T., Yasunishi, A.,
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High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-reseasc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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192 ggagatriargaigteeeeyygaleegeeegleeacceeaacggeacteleeaaalttt
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GTGCCTCATCCCCTCTTCAGTGCAGGAATACGTTAGCGTCGTGTCTTGGGAGAAAGACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     further details.
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/clone_jjb="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1 366 c 349 g 297 t
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/strain="C57HL/6J"
/dh_xref-"taxon:10090"
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/db_xref="MGD:MGI:1918065"
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/sex="male"
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                                                                         cgggaccaggacgggatttatggcaaagcaytcatcctcaattgttctgctqagggttac 2148
ATTGCCCTGAATGCCAGAATCCAGGTCCTGAGTAATGGCTCACTCTTGATCAAGCATGTT 288
                                                                                                                                                    CGGGACCAGGATGGGATTTATGGCAAAGCAGTGATTCTCAATTGCTCTGCAGAGGGTTAT 408
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Norway rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa Tel: 319 335 8250
Fax: 319 335 9565
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BF565509.1 G1:11675287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID- 1799773 The following
repetitive elements were found in this cDNA sequence: 68-149,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      discovery
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria;
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Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                            /lab_bost="bHIOB" (Life Technologies)"
/lab_bost="bHIOB" (Life Technologies)" with a modified /note="vector: pf7T3D-Pac (Pharmacia) with a modified /note="vector: pf7T3D-Pac (Pharmacia) with a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
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/db_xref="taxon:10116"
/clone="U1-R-BT1 - akm f 08-0-U1"
/clone_11b="U1-R-BT1"
/dev_stage="adult"
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90.48;
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Pred. No. 3.1e-53;
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Contact: Yoshin.de Hayashizaki
Laboratory for Genome Exploration Research Group. RIKEN Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
, Y., and Hayashizaki, Y.
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Thermostabilization and thermosetivation of thermolabile enzymes by
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/dev_stade="10 days neonate"
/lab_host-"DHIOB"
/note="Site_1: Sall; Site_2: Bam
                                                                                                                       medulla oblongata*
                                                                                                                                                       /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                 /clone="B830046F24"
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## SUMMARIES

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2. AL CENT.	7.					Idilifera	o litions	on molecule; ental retarda agenesis; human; ds; ss	Down syndrome-cell adhesion molecule DS-CAMI			04 BP.	ALIGNMENTS	AAQ65674	AAH99637	AAI61182	AA159396	AAF30917	AAC23431 AAC12752	AAQ80196	AAC90961	AAQ86902	AAF44662	AAZ363Z1	AAZ36322	AAZ36301	AA051015	AAQ51017	AAX57250	AAX55767	AAS22684	AAH98405	AAZ91908	AAA88739	AAD10107	AAS02144	AAT85389	AAQ86478	AAH14602
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AAV31988 1D AAV3

AAV31988

standard;

CUNA;

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atglqqalartgqctctctcctlgttccagagcttcgcgaatgttttcagtgaagaccta

Matches

Similarity

100.0%;

Score 4678. Pred. No. Mismatches . 0; DB 2 19;

Length

6413; 0,

Gaps 60

0

0;

Conservative

Sequence

6413

BР;

1633

Α.

1781 C; 1707 G; 1292 T;

0

other

RESULT

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destation) chan library. Further, check were obtained by exon CC trapping, and the complete PS CAM2 chan sequence was identified.

CC DS-CAM2 is a splice variant of membrane-bound DS-CAM1 (see AAM42086) CC and is deleted for the entire transmembrane domain. The DS-CAM CC gene spans youl-1200 kb of genomic DNA and maps at chromosome CC 1922.2-22.3. The invention also provides murine DS-CAM partial CC transgenic animals, antisense oligonucleotides, and primers useful CC for amplification of DS-CAM nucleic acid. DS-CAM polypeptides are CC associated with developmental and neurological processes. They can CC methods of repairing (regenerating) damaged or severed peripheral CC nerves. The products can also be used in detection, diagnosis and CC methods of repairing (regenerating) damaged or severed peripheral CC compus callosum, or schizenephaly. Antisense oligonucleotides of the corpus callosum, or schizenephaly. Antisense oligonucleotides CC are used for inhibiting translation of mRNA.
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holoprosencephaly; corpus callosum agenesis;
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                                                                                                                                                                                                                                                                                                                                  DS-CAM2 (see AAW42087), an extracellular, soluble protein belonging to a novel subclass of the 1g superfamily with highest homology to neural cell adhesion molecules. A modified direct cDNA selection technique was applied to bacterial and Plartificial chromosomes between ETS2 and MXI by using cDNA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental and neurological abnormalities
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DS-CAM2 (see AAW42087),
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141   gegentaccagggattcar~cacgaasaccttataatggatcacatggtcaaaagtgacggiistigtegacatggtcaaaagtgacggiistigtegacgiistigtegacggiistigtegacggiistigtegacggiistigtegacggiistigtegacggiistigtegacggiistigtegacggiistigtegacggiistigtegacggiistigtegacggiistigtegacggiistigtigtiiiiiiiiiiiiiiiiiiiiiiiiiii

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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
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14-SEP-2000;
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29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-2001
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Wang
Zhao
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                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                       chemokinetic;
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                                   Novel nucleic acids such as central nerv
                  Claim 1;
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Wang Z,
Zhou P,
                  SEQ ID NO 399; 10078pp; English.
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2000US-0598042
2000US-0620312
2000US-0653450
2000US-0662191
2000US-0693036
2000US-0727344
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                                     nervous
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Wehrman T, 1
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                                     polypeptides, useful system injuries -
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Yang Y,
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Zhang
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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful ingene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotractic/chemokinetic activity, haemostatic activiny, inhibit activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constraints.
                                                specification
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Query Match Sequence 38.6%; Score Pred. NO. 0; DВ Length

Mismatches 1422;

Indels

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Gaps

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                                                                                                                                                                                                                                    This cDNA sequence comprises the 5' region of a cDNA clone for murine bown syndrome cell adhesion molecule (DS-CAM), a member of a novel subclass of the 1g superfamily with homology to neural cell adhesion molecules. The middle region (see AAV31986) and 3' region (see AAV31987) of the clone are also provided. The murine DS-CAM clone was isolated from a C57 Black/6 mouse brain cDNA library using human DS-CAM clone (see AAV31988) as
                                                    cDNA library using nument by construction (see probe. The invention also provides human DS-CAM proteins (see probe. The invention also provides human DS-CAM proteins (see AMW42086-87), as well as expression vectors and host cells. ARW42086-87), as well as expression vectors and host cells. ARW42086-87), as well as expression vectors and primers useful transgenic animals, antisense oligonucleotides, and primers useful conspicuous description of DS-CAM polypeptides are associated with developmental and neurological processes. They can be used in entubulation be used in entubulation methods of repairing (regenerating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and therapy of developmental and neurological abnormalities such as Down syndrome, mental retardation, holoprosencephaly, agenesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Down's Syndrome-cell adhesion molecule develop products for detection, diagnosis and therapy developmental and neurological abnormalities
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                                                                   Secreted protein; membrane-associated protein; protein secretion; signal peptide; alkaline phosphatase; ptrAP3; neural adhesion; ethb0018f2; ss.
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CC brain cDNA using a novel method for identifying genes encoding to movel secreted or membrane-associated proteins. The method comovel secretal (i) liquing a library of cDNA to DNA such as vector comovers (i) liquing a library of cDNA to DNA such as vector comovers (ii) that lacks comovers peptide and membrane anchor sequences (see AAW55047); (ii) comovers and peptide and membrane anchor sequences (see AAW55047); (ii) comovers and comovers (some of) the bacterial clones into mammalian comovers and comovers and (v) identifying a clone in the commandation of the bacterial library, isolating the corresponding clone in the bacterial library, isolating the corresponding clone in the bacterial library, isolating the corresponding clone in the bacterial library, associated (see as a partial cDNA clon of a movel neural addression molecule (see consecutive liquid) and comovel method is very sensitive and is suitable for high throughput consecuting techniques and automation.
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Best Local Similarity 62.16

Matches 844: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   murine DS-CAM clone was according to the problem of provides human DS-CAM proteins (see probe. The invention also provides human DS-CAM proteins (see probe. The invention also provides human DS-CAM proteins (see probe. The invention also provides human DS-CAM proteins (see probe. The invention also provides and host cells, transgenic animals, antisense oligonuclocitides, and primers useful transgenic animals, antisense oligonuclocitides, and primers useful for amplification of DS-CAM nucleic acids. DS-CAM polypeptides for amplification of DS-CAM nucleic acids. DS-CAM polypeptides for amplification of DS-CAM nucleic acids.
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                                                                                                                                                                                                                                                                                                                                             associated with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (remembrating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and therapy of developmental and neurological abnormalities such as pown syndrome, mental retardation, holoprosencephaly, agenesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides
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                                                                                   tgataacatcctatccaaaatactaccctggccacgcaggggcaggaaaaaggagatgagct 2425
                                                                                                                                                       aacyatgtyggcqcaga--cgtcagcaagtccatgtacctcacggttaaaattcctgcga 2365
GCACAGCCCATG--GGAGAGCCCATCATTGTCCGCT-GGAGAAGAGAGACAGGATCATTA 722
                  gcacygcqcatggtgagaagcccattatagtccqctgggagaaggaaggacgaatcatta 2485
                                                                AACGATGTGGGCGCAGAACGTTCAGCAAGTCCATGGACTCACAGGGAAA-----TTCCGG 838
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5.5e-136;
nes 135;
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                                                         holoprosencephaly;
                                                                   signal transduction;
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                                               ly; corpus callosum agenesis; diagnosis; assay; mouse; ds;
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CC for murine Down syndrome-cell adhesion molecule (DS-CAM), a CC member of a novel subclass of the 19 superfamily with homology to CC neural cell adhesion molecules. The middle region (see AAV31986) CC and 5' region (see AAV31985) of the clone are also provided. The CC murine DS-CAM clone was isolated from a C57 Black/6 mouse brain CC cDNA library using human DS-CAM cDNA (see AAV31981) as CC probe. The invention also provides human DS-CAM proteins (see CA AAV42086-87), as well as expression vectors and host cells, CC transgenic animals, antisense oligonucleotides, and primers useful CC associated with developmental and neurological processes. They can CC methods of repairing (regenerating) damaged or severed peripheral CC metros. The products can also be used in detection, diagnosis and CC therapy of developmental and neurological abnormalities such as CC Down syndrome, mental retardation, holoprosencephaly, agenesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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                                                                                                                     The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with mootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays the suppression of the activity, arthritis and inflammation, leukaemias and
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Wang Z,
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                                                                                                                                                                                                                                                                                                                                           Human Down syndrome-cell adhesion molecule DS-CAM probe E51.
                                                                                                                                                                                                                                                                                                signal transduction: trisomy 21; mental reta
holoprosem cephaly; corpus callosum agenesis;
                                                                                                                                                                                                                                                                                                                       DS-CAM1; Down syndrome-cell adhesion molecule; neural cell;
                                                                                                                                                                                                                                                                                                                                                                   28-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                        AAV31982;
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                                                                                                                                                                                                                                             W09817795-A1.
                                                                                                                                                                                                                                                                                      schizencephaly; diagnosis; assay; human; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238
This polynucleotide comprises cDNA fragment E51 that was isolated from a human trisomy 21 toetal brain (14-wk gestation) cDNA library following a modified direct cDNA selection technique
                                                               New isolated Down's Syndrome-cell adhesion molecule -develop products for detection, diagnosis and therapy developmental and neurological abnormalities
                                                                                                                                                                                                                        30-APR-1998
                                                                                                                                                                                                                                                                 Homo sapieus
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                                                                                                           WPI; 1998-271791/24.
                                                                                                                                                                             25-OCT-1996;
                                                                                                                                                                                                   23-OCT-1997;
                                           Example 2;
                                                                                                                                  Korenberg
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                                                                                                                                                                                                   97WO-US19547.
                                           79; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                             cDNA;
                                                                                                                                                         MEDICAL CENT
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                                                                                                                                                                                                                                                                                                                mental retardation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and neurological processes. The polypeptides and nucleic acids are used to develop products for the detection, diagnosis and therapy of developmental and neurological abnormalities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 388 BP; 83 A; 119
                                                                                                                                                                                                                                                                                                                                                      wound
                                                                                                                                                                                                                                                                                                                                                          allergy; cancer; cardiovascular disorder;
wound healing; infectious disease; neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH24799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH24799 standard; DNA;
                    Nucleic acids encoding 2 human cytokine receptor-like polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers,
                                                                                                                                                         03-DEC-1999;
                                                                                                                                                                                                             07-JUN-2001
                                                                                                                                                                                                                                      WO200140456-A1
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide
            cardiovascular and immune disorders
                                                                                                      Ruben
                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                 30-NOV-2000; 2000WO-US32525
                                                                                                                                                                                                                                                                                                                                                                                igG Fc region; cytokine receptor-like protein; immune system disorder;
inflammatory disorder; immuno modulation; immune cell stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328
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                                                                             2001-367808/38
                                                                                                                                                                                                                                                                                                                                                      healing; infectious
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                                                               AAB84252
                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of a human cytokine receptor-like protein.
                                                                                                     Ni J, Young
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/*tag= a
/product= "cytokine:
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                                                                                                                                                                                                                                                                                                                                                         angiogenic disorder;
disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a human cytokine receptor-like protein. The cytokine receptor-like polypeptides and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3209 connected of the transplantation can be accorded against the second transplantation of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 906
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388;
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88; Conservative
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                                                                                                                                                                                                                                                                                                                              AAD05447
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation; allergy; neurological disorder; Alzhelmer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angioqenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gastrointestinal disorder; pregnancy-related disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD05447 standard;
          AAD05389-AAD05473 represent cDNAs corresponding to 29 human secreted protein genes, and AAE01546-AAE01630 represent the proteins they encode AAE01631-AAE01660 represent human secreted protein fragments or variants
                                                                                                                                                                                                                                                                                                                              WO200134623-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding partner
                                                                                                                                                                                                                                     05-NOV-1999;
30-JUN-2000;
                                                                                                                                                                                                                                                                            01-NOV-2000; 2000WO-US30037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endocrine disorder; infection;
                                                              Claim
                                                                                                                                              P-PSDB;
                                                                                                                                                                                                             ( - AMUH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune system disorder; AIDS; autoimmune disease; rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                         2001-316490/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein-encoding
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ting, diagnosing a
e and diabetic ret
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                                                                                                                                                                                                           HUMAN GENOME SCI INC
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                                                                                                                                                                                   Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                     99US-0163577
2000US-0215137
proteins
                                                              457-459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; proliferative diso der;
                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
1388..1413
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                        /partial
1297..1387
                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human
/note= "CDS does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        /product- "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental abnormality; haematopoietic disorder;
                                                                                          retinopathy
 and
                                                                                                                                                                                   GA,
                                                              535pp; English.
                                                                                                      and/or treating
                                                                                                                  29 human secreted polypeptides, useful
their genes
                                                                                                                                                                                      Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene 17 cDN/ clone HHSFB67,
                                                                                                                                                                                                                                                                                                                                                                                                                                     not
                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted protein*
not include start codon*
                                                                                                                                                                                       PA;
  are useful
                                                                                                      e.g. cancers, Parkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO:69
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skin disorders (e.q., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antil odles specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and indiagnostic immunoassays e.g., raijoimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human for the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 29 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic dischers, diseases of the immune system, and the statement of the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammat allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, compare disease, schizophrenia, asthma, asth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating or ameliorating medical conditions, e.g., by protein or therapy. Pathological conditions can be diagnosed by determining
                                                                                                            protein-encoding
      766
A; 1190
                                                                                                                  CDNA of
C;
      1357
                                                                                                                        the invention.
      ç;
            1009 T;
            14 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation,
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Sequence 4336 BP; 766 A; 1190 C; 1357 G; 1009 T; 14 other;

Query Match
2.08; Score 91.4; DB 22; Length 4336;

Best Local Similarity 45.98; Pred. No. 1.3e-15; Todals 6: Gare

2;

Matches 3152 3032 3209 ccaycuur la---geteaccalcacygeggacgaggegetectgatggtecacctcagg 2968 AGCCCTTCACGTCCTACAAGTTCCCAAGTGAAGGCGACCAATGACATTGGCGACAGCGAGT 3093 accetterteraecteragealceqealgtacyceaagaaceggattggcaagagegage 2911 daCalifiqeaaaafqqadfafeeqfqqetaeeaaafaqgttaeeggagagtaeagcaetg 3088 TCCTCTCCCTGACGCCCACACCACCACCACCTCCGTGCTAATCCGATGGCAGCCGCCAGCAG 2973 aagttcacctqqaqcctatarcatcacagagcatcagggtcacatggaaggctcccaaga 3028 ccqqcacqqygyccttcttctcaggaaatcatcaccaccactctcgaggatgtgcccagtt 3268 --CTTACCTACCTGAACAAGCACAGGCGGTACGAGATACGGATGAGCGTGTACAACGCTG ccctqqacaacctgaataaqttcactcaqtacqgcctggtggtggaggcctgtaaccggg 3208 AAGGACTGAGGGGCTTCACGCTTCGAGGCATCAACAACCCAGGGGCCACATGGGCTGAG TCAGCGAGGAGTCGGAG CAGCACCTCGTAACGTGGTCGTCCACGGCGCCACGGCCACACAGCTGGACGTGACTTGGG acccccccgaaaatglccaagccatagcaacatcaccagaaagcatatcaatatcctggt 3328 AAGCCCAGCGGGGGAACCTCACAGAGCGAGTGAAGACGCTTTTCCTGGCTGAGAACAGCG ccaacctcatggacggagagctgggtgagattaaaaacatcaccaccaccacagccttcac ccacactttccaaggaagccttgaatggaattctccaaggggttcagagtcatttactggg TGGGTGAGGGGCCCTCCAGCCCCCCCCGCAGGAGGTCTTTGTTGGGGGAGGCAGTGCCCACAG 388; Conservative INCTIGACCACCCTGCAGGCTGCCCCCGATGAAGCACCCACCA 3033 0; Mismatches 451; Indels 6; Gaps 2852 2913 2616 2676 2736 2796

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27-AUG-1999;
11-JAN-2000;
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprimertary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a sequence and an oligonucleotide comprises a si'-end sequence where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH06899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA clone (5'-primer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000;
                                                                                                                                                                                                                                            primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                (HELI-) HELIX KES
                                                                                                                                                                                                                                                                                                         WPI; 2001-318749/34.
                                                                                                                                                                                                   Claim 1; SEQ
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full-length
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C, Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises as sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection, and/or diagnosis of the abnormality of the proteins encoded by the
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09-JUN-2000;
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gcggggacagtgaggtttacaccctggacaacctgaataagttcactcagtacggcctgg
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                                tecgatggeageegeeageagagacaagateaatggeateeteetgggetteeggatee
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                                                                                                                                                                                                                                                                                        present invention.
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, Sugiyama
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; 2000JP-0183767.
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T, Wakamats
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Protein yrosine phosphate protein PTP-OB specifically expressed in bone cells - modulators of which are used to treat, e.g. osteoporosis, and prevent and treat bone loss and cancer.
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Perfect score:
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Maximum DB seq length: 200000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Maximum Match 1008
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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4 US-09-158-657-6

5 PCT-US94-10.166-6

5 PCT-US94-10.166-6

5 PCT-US94-10.166-6

2 US-08-327-497E-1

2 US-08-327-497E-1

2 US-08-427-497E-1

2 US-08-427-497E-2

2 US-08-447-464-2

2 US-08-447-464-2

2 US-08-08-166-2277-1

1 US-08-08-485-1

1 US-08-08-666-392A-1

2 US-08-746-559A-1

2 US-08-746-559A-1

2 US-08-746-559A-3

2 US-08-036-210-21

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2 US-08-035-08493-18
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ALIGNMENTS	35	35	36.2	36.2	36.6	36.8	38	39	39	39.2	39.2	39.2	40.6	40.6	40.6	40.6	40.8	41
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	US-08-894-818B-14	US-08-750-532-11	US-08-644-271-2	US-08-374-834-2	US-08-427-497E-5	US-08-737-715-1	US-09-383-586-24	US-09-244-796-17	US-09-007-005-17	PCT-US95-04681-10	US-08-702-367A-10	US-08-449-645A-10	US-08-040-741-5	US-08-714-901-5	US-08-408-420A-5	US-08-408-093-5	US-08-232-463-14	PCT-US95-08493-20
	Sequence 14, Appl	Sequence 11, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 24, Appl	Sequence 17, Appl	•	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appl1	Sequence 5, Appli	Sequence 14, Appl	Sequence 20, Appl

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RESULT 1
US-08-752-307B-6
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NAME: Meiklejohn, Ph.D., Anit.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 0940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
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APPLICANT: McCarthy, Sean A.
APPLICANT: Gearing, David P.
APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/01
FILING DATE: 19-NOV-1996
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastsE0 for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1493 base pair
                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                          FEATURE:
NAME/KEY:
LOCATION:
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CITY: Boston
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                                       CCTGACACCAAAGAAGCTGAAGACCGGCATTGGCAGCACGGTCATCCTCTCCTGTGCCCT
                                                  catcagtcccaggaaggttaaaagcagcgtgggtagccaagtttccttgtccttgcagcgt 1010
                                                                             CACCTTCGGCTTCGGCAGAGGCCACAGGCATCCTCATGGTCATTGATCCCCCTTCATGTGAC
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34; Conservative
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Pred. No. 4.8e-150;
0; Mismatches 508;
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US-08-348-006B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08348006B Patent No. 5658756 GENERAL INFORMATION:
                                                                                       TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: li
MOLECULE TYPE:
)8-348-0068-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1472 GTACACCATGTCGGACGGCACC
                                                                                                                                     NAME: HAND, J., MARK
REGISTRATION NUMBER: 18,545
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
ETLING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 07065-0900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 126
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                               STRANDEDNESS: single
                                                                              LENGTH: 6000 base pairs
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126 E. LINCOLN /
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                                  linear
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Query Match

1.48;

Score 66.4;

DB 1;

Length 6000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                         ATTORNEY AGENT INFORMATION:
NAME: HAND, J. WARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
             TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF CONTROL OF THE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: J. MARK HAND - MERCK & CO., INC
ADDRESSEE: J. MARK HAND - MERCK & CO., INC
ADDRESSEE: J. MARK HAND - MERCK & CO., INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 14-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: RAHWAY
STATE: NEW JERSEY
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: RUTLERGE, SU JANE
TITLE OF INVENTION: CUNA ENCODING A NOVEL HUMAN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
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                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2141 GTGCCCAGCGCGCCGCGGAAGGTGGAGGCGGAGGCGCTCAACGCCACGGCCAT 2196
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                        SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROBAN, GIDEON A.
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   STATE: N
                                                                                                                                                                                                                                                                ADDRESSEE: J. MANN ...
                                                                                                                                                                                                      ZIP: 07065-0900
                                    CLASSIFICATION:
                                                     FILING DATE
                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                            CITY:
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                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                           J. MARK HAND - MERCK & CO., INC 6 E. LINCOLN AVE., P.O. BOX 2000
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Pred. No. 2.6e-09;
0; Mismatches 246;
                                                                                                           Version
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ATTORNEY/AGENT INFORMATION:

14-FEB-1997

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; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-09-158-657-6
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PCT-US94-10166-6
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                                                                                                                                                                                                                                                              Sequence 6, Application PC/TUS9410166 GENERAL INFORMATION:
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NAME: HAND, J. MARN
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1899
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3145 tacaccctggacaacctgaataagttcactcagtacggc:tggtggtgcaggcctgtaac 3204
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                                                                                                                                                                      APPLICANT: RODAN, GIDEON A
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                        2141
                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W WALLEN III
STREET: P.O. BOX 2000, 126 E.
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                 COUNTRY: U
ZIP: 07065
                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgggccggcacggggccttcttctcaggaaatcatcaccaccactctcgaggatgtgccc 3264
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                                                                                    RAHWAY
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                                                    USA
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Pred. No. 2.6e-09;
                                                                                                        E. LINCOLN AVE
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US-08-427-497E-4

Sequence 4, Application Patent No. 5969124 GENERAL INFORMATION:

US/08427497E

2140

APPLICANT: Lemmon, TITLE OF INVENTION:

Vance

A Method for Characterizing the

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Best Local Similarity 47.7%;
Matches 227; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1721 TACGTGGTGGAGGACCTGAAGCCCAACACGGAGTACGCCTTCCGCCTGGCGGCCCGCTCG 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3145 tacaccctggacaacctgaataagttcactcagtacggcctggtggtggtggcaggcctgtaac 3204
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TELEFAX: 138825
   2141
                      3562 gttccaggtcctcccgcgggtgtgaaggcagcggcggcctcagcctccatggtctt 3617
                                                                                                                                         2021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US94/10166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
GTGCCCAUCGCGCCGCGCGAAGGTGGAGGCGGAGGCGCTCAACGCCACGGCCAT 2196
                                                                  CACACAGAGGTGGGACCAGGGCCCGAGAGCTCGCCCGTGGTCCTCCGCACGACGAGGAT
                                                                                        ttcacccggcaggagacggqqtcaggagtgagcagatcttcacccggaccaaagagggat 3561
                                                                                                                                    TGGCGCCCGCCGCCGGAAACGCACAACGGGGCCCTGGTGGGCTACAGCGTCCGCTAC
                                                                                                                                                                                                                                                                                                  tggtccacactttccaaggaagccttgaatggaattctccaggggttcagagtcatttac 3384
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pred. No. 2.6e-09;
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25
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Patent No. 5969124
TITLE OF INVENTION:
TITLE OF INVENTION:

TITLE OF INVENTION:

Nucleotide Sequence of L1CAM

the Nucleotide Sequence Characterized Thereby

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                                                                                            Matches
                                                                                                           Best
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: June 26, 19 ATTORNEY/AGENT INFORMATION:
                                1555 TATACCTCCTACCACCTGGAGGTGCAGGCCTTTAACGGGGCGAGGATCGGGGCCCCGCCAGC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
3532 gagcagatcttcacccggaccaaagaggatgttccaggtcctcccgcqgqtgtgaaggca 3591
                                                   3472 tacaccaactacagcatccaggtgctggccttcacccgcgcaggagacggggtcaggagt 3531
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                            JOURNAL: --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Suite 70
CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/427,497E FILING DATE: April 24, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07 FILING DATE: June 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 24,175
                                                                                            Local Similarity nes 119; Conser
                                                                                                                                                                                                                 PAGES:
                                                                                                                                                                                                                                                                           AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing of
TITLE: human L1CAM: an interspecies comparison.
                                                                                                                                                                                                                                                                                                                                                                     LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Minnich, Richard J.
                                                                                                                                                                                                                                   ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRY: U.S.A.
44114-2518
                                                                                                                                                                                                   : 416-423
1991
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                                                                                            Conservative
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                                                                                            0;
                                                                                                           Score 47.8;
Pred. No. 0.
                                                                                              Mismatches
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 435
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/
APPLICATION NUMBER: 26, 71
                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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ANTI-SENSE: no
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (216) 861-5582
                PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                      IMMEDIATE SOURCE
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STREET: Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Compaq Prolinea 5100e OPERATING SYSTEM: DOS 5.0
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                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR
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                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                     INDIVIDUAL ISOLATE:
                                                                                                                                         ORGANISM:
                                                                                   LIBRARY:
                                                                                                                                                                                                                                                                                   LENGTH:
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Molecular structure and functional testing
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                                                                                                                                                                                                                                                                                                                                                          (216) 241-1666
                                                                                   Stratagene cDNA Library 936206
                                                                                                                       homo sapiens
ISOLATE: 17-18 week fetus
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Characterized Thereby
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Nucleotide Sequence of LICAM
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Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5872225
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APPLICANT: Lemmon
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: storable
                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9.
FILING DATE: June 26, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                              NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGES: 416-423
DATE: 1991
RELEVANT RESIDUES IN SEQ ID
                                                                                                                                                                                                                                                                             COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 44114-2518
                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Cleveland
STATE: Ohio
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                                                                                                                                                                                                         APPLICATION NUMBER: US/08/341,843B FILING DATE: No. 5872225ember 18, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 Superior Avenue STREET: Suite 700
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6, 1992
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Pred. No. 0.00073;
""Fmatches 97;
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                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08427497E Patent No. 5969124
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Best Local Similarity
                                                                                                                                                                                                       Patent No.
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                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: Stratagene cDNA Library 936206 CLONE: synthesis of 4 clones PUBLICATION INFORMATION:
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LIBRARY: Strate
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MOLECULE TYPE: CDWG
MOLECULE TYPE: CDWG
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                                                                                                                                       NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                      APPLICANT:
COMPUTER READABLE FORM
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                                                         STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
               COUNTRY: U.S.A. ZIP: 44114-2518
                                                                                                       ADDRESSEE: Fay, Sharpe, Beall, Fagan
ADDRESSEE: Minnich & McKee
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1991
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                                             Ohio
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Characterized Thereby
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Pred. No. 0.00082;
0; Mismatches 97;
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RESULT 10
US-08-427-497E-2
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: Stratagene cDNA Library 936206
CLONE: synthesis of 4 clones
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: June 26, 19 ATTORNEY/AGENT INFORMATION: NAME: Minnich, Richard J
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                  3532 gagcagatetteaceeggaecaaagaggatqtteeaggteeteeegggggtgtgaaggea 3591
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MOLECULE TYPE: nucleic ac
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APPLICATION NUMBER: (
                                                                     2839 GTGCTCACCGGCTACGTGCTCTCCTACCACCCCCTGGAT 2877
                                                                                          3652 atcatccgaaagtacactgtattctgctcccacccctat 3690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE: Molecular structure and functional TITLE: testing of human LICAM: an TITLE: interspecies comparison.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/427,497E FILING DATE: April 24, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb MEDIUM TYPE: storable
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Hlavin, Mary Louise AUTHORS: Lemmon, Vance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
INDIVIDUAL ISOLATE: 17–18 week fetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISSUE:
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                                                                                                                                           GAGTGCCAGTCGAACACCAGCCTGCTGCTGCGCTGGCAGCCCCCACTCAGCCAACGGC
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Pred. No. 0.00082;
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Query Match 1.0%; Best Local Similarity 54.3%; Matches 119; Conservative

Score 47.8; DB 2; Pred. No. 0.00082; 0; Mismatches 97;

Length 3774; Indels

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Gaps

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; RELEVANT RESIDUES IN SEQ ID US-08-427-497E-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (216) 241-16
TELEX: (216) 980162
INFORMATION FOI SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWITTELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERIST 'S:
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NAME: Minnich, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                                                                                                       LIBRARY: SURCE:
                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/41 FILING DATE: April 24, 1995
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OPERATING SYSTEM: DOS 5.0
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                                  PAGES:
                                                                                                                AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing
TITLE: human LICAM: an interspecies comparison.
                                                                                                                                                    AUTHORS: Hlavin, Mary Louise AUTHORS: Lemmon, Vance
                                                                                                                                                                                                                                                         ORGANISM: Homo Sapieus
INDIVIDUAL ISOLATE: 17-18 week tetus
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                                                                                    VOLUME:
                                                                                                 JOURNAL:
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                                  1991
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Minnich & McKee
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                                                                                                                                  ; LOCATION:
US-08-447-464-2
                                                Query Match 1.0%;
Best Local Similarity 51.7%;
Matches 104; Conservative
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                                                                                                                                                                                                                                                        TELEFAX: 212-869-8864/9/4J
TELEX: 66141 PENNIE
INFORMATION FOR SEK ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5690 wase pairs
`3455 tggacgggctygaaaagtacaccaactacagcatccaggtgctygccttcacccgcqcag 3514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: JBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-MAY-1995
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                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                    TYPE:
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                                                                                                                                                                                                                                     unknown
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                                                    Score 45.8; DB 2;
Pred. No. 0.0044;
0; Mismatches 97;
                                                                                   Length 5690;
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US-08-716-679-2
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US-08-716-679-2
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Patent No. 5846800
                                                                Query Match
Best Local Similarity
Matches 104; Conserv
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                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-1-N-S/MS-DOS
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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APPLICATION NUMBER: US/08/130,570
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                3455 tgqacquqctggaaaagtacaccaactacagcatccaggtgctggccttcacccgcgcag 3514
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ATTORNEY/AGENT INFORMATION:
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2256 TGGGCAGCTGCTAGAGGATGAGACCTACACTGTGAGAGTGCTCGCCTTCACATCGGTGG 2315
                                                                                                                                                                                                                               MOLECULE TYPE:
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TELEFAX: 56141 PENNIE
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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10036-2711
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                                                                                                                                                                                                                                                                                 nucleic acid
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nilarity 51.7%;
Conservative
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                                                                                                                                                                                                                                                                unknown
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                                                                  Score 45.8; DB 2;
Pred. No. 0.0044;
0; Mismatches 97;
                                                                                                   DB 2;
                                                                                                     Length 5690;
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                                                                                                                                                                              Matches
                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bredesen, I
APPLICANT: Rabizadeh,
TITLE OF INVENTION: PI
TITLE OF INVENTION: PO
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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3264 cagttacccccccccaaaatgtccaagccatagcaacatcaccagaaagcatatcaatatc 3323
                                                                                3204
                                                                                                                1746
                                                                                                                               3144 ttacaccctygacáacctyaataagttcactcagtacggcctggtggtggtggaggcctgtaa 3203
                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                                                   TTATAAACTGGAAGGCCTGAAAAAATTCACCGAATATAGTCTTCGATTCTTAGCTTATAA 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24, Application US/09041886
o. 6235872
                                                  TCGCTATGGTCCGGGCGTCTCTACTGATGATATAACAGTGGTTACACTTTCTGACGTGCC
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bredesen, Dale E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States
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Polypeptides and Methods of Use
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Pred. No. 0.0058;
0; Mismatches 118;
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                                                                                                                                                                                               2; DB 4; Lenyth 4608; 0.0058;
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PCT-US94-05277-1
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PCT-US94-05277-1
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GENERAL INFORMATION:
                                                                                                                                     Query Match
Best Local Similarity
Matches 116; Conserv
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NAME: Kayan, Sarah A.
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                     3204
                                                                     1746
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1806 TCC TRATEGTCCGGGCGTCTCTACTGATGATATAACAGTGGTTACACTTTCTGACGTGCC 1865
                                                                                       3144 ttacaccctygacaacctygataagttcactcagtacggcctggtggtgcaggcctgtaa 3203
                                                                                                                                                                                                                                                                           FEATURE:
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US94/05277
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                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                             CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                ccugaccuacacagagacettetteteagaaaateateaceaceactetegagaatgtgcc 3263
                                                                  TTATAAACTGGAAGGCCTGAAAAAATTCACCGAATATAGTCTTCGATTCTTAGCTTATAA 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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1001 G Street, N.W.
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VENTION: Antibodies Specific for DCC Gene Product
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                                                                                                                                       Conservative
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                                                                                                                                     Score 45.2; DB 5;
Pred. No. 0.0058;
0; Mismatches 118;
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RESULT 15
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TELECA: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4843 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08986485 Patent No. 6046030
                                                                                                                                                                                                                                  Query Match 1.0%;
Best Local Similarity 50.9%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: WU, SHUJIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUNCH, ALEMSEGED
TITLE OF INVENTION: A HUMAN 1.1G-1 HOMOLOG (HLIG-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IHM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER 6 PRESTIA
STREET: P.O. BOX 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
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MEDIUM TYPE: Diskette
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                                                                              2183
                                                                                                                                                           2123 CCCCATCCTTGGTGGTCCCCCTTGGAAGACCGTGTGGTATCTGTGGGAGAAACAGTGGCCC 2182
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                                                                                                                                                                                 671 ccccatr atactggatggqtttgaccatcgcaaag catggctqggcagcgtgtggagc 730
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Search completed: March 4, 2002, 05:11:29 Job time: 16943 sec

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BI102963 602888573
AL182061 Tetraodon
AW176762 RCO-CT009
AV158019 AV158019
AI422998 tf31b11.x
AI927023 wo87a06.x
AW78073 6184f06.y
N24917 yy01h12.s1
AW015308 UI-H-BIO-
                                                                                                                                          Description
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## REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION RESULT BF348620 COMMENT FEATURES JOURNAL source Mammalia; Eutheria; Prim. tree; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 744) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (Mational Institutes of Health, Mammalian Gene Collection (Mammalian Gene Collection (Mational Institute Gene Collection (Mational Institute Gene Collection (Mational Institute Gene Collection (Mammalian Gene Colle BF348620 : 4 bp mRNA EST 22-NOV-2000 60201:924F1 NCI\_CGAP\_Brn67 Homo sapiens cDNA clone IMAGE:4155508 5', magazioca DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9426 row: p column: 05 High quality sequence stop: 697. Location/Qualifiers. Homo sapiens Eukaryota; M human BF348620.1 GI:11296215 BF348620 /organism-"Homo sapiens" /db\_xref-"taxon:9606" /clone-"IMAGE:415508" /clone\_lib-"NCI\_CGAP\_Brn67" /tissue\_type-"anaplastic oligodendroglioma with lp/19q Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Prim. + --; Catarrhini; Hominidae; Homo. Gene Collection (MGC) ğ

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19; Conser
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Plate: 88 row: K column: 9
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                       Bmail: smith@email.marc.usda.gov
Single pass sequencing. Bases called
v0.980904.e. Vector identified by cro
and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 538)
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Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Design and use of two pooled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A.,
                                                                                                                                                                                                                                                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT
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/note="Organ: brain; Vector: pCMV-SPORF; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 196 c 210 g 150 t
                                                                                                                                                                        /note-"Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
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                                                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DH10B"
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/clone_lib="MARC lPIG"
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
below when ordering this clone: Source lab clone id - xinngaOlie19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Other_ESTs: dg39c10.xl
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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High quality sequence stop: 439.
Location/Qualifiers
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizan
Bouneau, L., Billault, A., Quetier, F., Saurin, W.,
Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                       Eukaryota; Metazoa; Chordata; Crania a; Vertebraia; Ente ostomi; Actinopterygii; Neopterygii; Teleostri; Euteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                  Weissenbach, J
                                                                                                                                                                                                                                                                                                                            CNS025H0 832 bp DNA GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 236J16 of library G from Tetraodon nigroviridis, genomic survey
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18; Conserv
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Tetraodon nigroviridis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI102963 739 bp mRNA EST 26-JUN-2001 60288573F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5043738 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1 (bases 1 to 739)
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Clone distribution: MGC clone distribution information can be
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/Clone=lib="NCI_CGAP_Kid14"
/Lab_host="DHHOB (Tl phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Site_2: Sall; Cloned unidirectionally. Primer: Oli Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. | " a 201 c 168 g 170 t I others
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/strain="FVB/N"
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Pred. No. 3.9e+02;
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                                                                              Dasilva, C., Fizames, C.,
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                                                                                                                           This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.p17t1=RCO&t2=RCO-CT0094-200899-002-812&t3-1999-08-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 177.
                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of
scale clone-end sequencing project of the Tetraodon nigrovi
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
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                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                           /clone_lib-"CT0094"
                         /dev_stage="Adult"
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/clone_lib="G"
/note="Genoscope sequence ID : COAG236DE08SP1-end
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221 c 168 g 202 t 5 others
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/db_xref="taxon:99883"
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                                                                                                                                                                                                                                                                                                                                                      Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998)) please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-1-1 Koyadai, Tsukuba, Tharaki 305-0074, Japan
Tel: 81-298-36-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN
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                                                                                                                                                                                                                                                                                                                                            details.
                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3010012H19"
                                                                                                                         /tissue_type="head"
/dev_stage="12-day embryo"
64 c 70 g 121 t
                                                                                                                                                                                 /sex="mixed"
                                                                                                                                                                                                    /clone_lib-"Mus musculus head C57BL/6J 12-day embryo"
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                            Score 16.8; DB 10; pred. No. 7.1e+02;
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1 (bases 1 to 334)

1 (NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1588 Std Error: 0.00 Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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A1927023 343 bp mRNA EST wo87a06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
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Location/Qualifiers
                                                                                                                                                                                                                                                                 85
                                                                                                                                                                                                                                                          /clone="IMAGE:2097789"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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/db_xref∸"taxon:9606"
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Pred. No. 7.1e+02;
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                                                                                                                                                                                                  Length 334;
                                                                                                                                                                      Indels
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      IMAGE: 2462290
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                    08-MAR-2000
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mRNA sequence.

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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., I
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., I
                                                                                                                                                                                                                                                                                                                                        AW780736 350 bp mrnn EST 112-MAY-2000 12-MAY-2000 EST 5184f06:y1 Gm-c1037 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1037-732 5', similar to TR:096305 Q96305 SIMILAR TO CIUTAREDUXIN ENCODED BY GENBANK ACCESSION NUMBER Z49699 ;, mrnn sequence.
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 444 Std Error: 0.00
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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Location/Qualifiers
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                                                                                  (bases 1 to 350)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-Torgan: kidney; Vector: pT7T3D-Pac Pharmacia) with a modified polylinker; Site_1: Not I; Si _2: Eco RI; Plasmid DNA from the normalized library HC1_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Shares and M. Fatima Bonaldo. The driver is a contraction by Bento Shares and M. Fatima Bonaldo. The contraction by Bento Shares and M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.8; DB 10;
Pred. No. 7.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 343;
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                                                   Khanna
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Matches 18; Conserv
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                                                           AUTHORS
                                                                                                                                                                   ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 356)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
                                                                                                                                                                                                                                                                                            N24917 356 bp mRNA EST 28-DEC-19901hi2.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE: 270023 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3322 PAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
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public Soybean EST Project
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to vector length is 351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linkers adapters were ligated to the blunt ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the psPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electro- Max DH10B host ceils. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of illinois at Urbana- Champaign. email: 1-vodkin@uluc.edu*a 46 c 65 g 146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone-"GENOME SYSTEMS CLONE ID: Gm-c1037-732"
/clone_lib-"Cm-c1037"
/tissue_Lype="fully expanded leaves of greenhouse grown plants"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLETE THE DEPORT; SITE_1: NOTI, SITE_2: SalI; This CONA library was constructed from mRNA isolated from full expanded leaves of greenhouse grown plants that were 2 weeks old. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restrictions site. SalI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Glycine max"
/db_xret-"taxon:3847"
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Pred. No. 7.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ccagttctcaaaggagcagg
oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                      AW015308 358 bp mRNA
UI-H-BIO-aap-e-04-0-UI.sl NCI_CGAP_Subl
IMAGE:2709991 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                     AW015308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stops: 29 Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,R., Williamson,A., Wohldma
The WashU-Merck EST Project
                                                                                                                                                            Tumor Gene Index
                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                      The sequence contained an oligo-dT track that was present in the
                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 358)
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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h quality sequence stop: 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino." 81 c 103 g 82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organisma"Homo sapiens"
/db_xref="CDB:3879665"
/db_xref="taxon:9606"
/clone="IMAGE:270023"
/clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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90.0%;
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Pred. No. 7.1e+02;
0; Mismatches 2;
                                    Soares Lab Clone distribution
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                                    AUTHORS
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Williams, J.,
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156 CCAGTCCCCAAAGGAGCAGG
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les 18; Conserv
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C84007 Dictyostelium discoideum SS
discoideum cDNA clone SSC227, mRNA
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Seq primer: M13 Forward
                                     Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H.,
                                                                                                                          Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
1 (bases 1 to 359)
                                                                                                                                                                                                          Dictyostelium discoideum
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1 79 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   יחסוס- "Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The
                                                                                                                                                                                                                                                                                                                                GI:2723613
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Takeuchi, I., Ochiai, H. and Tanaka, Y.
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Best Local Similarity
Matches 18; Conserv
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University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - 'Dictyostelium discoideum cDNA project in Japan'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development
DNA Res. 5 (6), 335-340 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hideko Urushihara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 380) ... NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
AI347190
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI347190.1
                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             numan.
                                                                                                                                                                                                                     Insert Length: 529 Std Error: 0.00
Seg primer: -40UP from Glbco
                                                                                                                                                                                                                                       www-bio.lln1.gov/bbrp/image/image.html
Insert Length: 529 Std Error: 0.00
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                                                                                                                                                                                  quality sequence stop: 337.
Location/Qualifiers
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/clone="SSC227"
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
/dev_stage="slug"
/dev_stage="slug"
57 c 68 g 119 t 1 others
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/note="Organ: colon; Vector:
modified polylinker; Site_1:
                                     /tissue_type="colon tumor, RER+"
/lab_host="DH10B"
                                                                          /clone="IMAGE: 2062902"
/clone_lib="NCI_CGAP_Co16"
                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 7.1e+02;
0; Mismatches 2;
      pT7T3D-Pac (Pharmacia) with
Not I; Site_2: Eco RI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 M-dical Center Dr., Rockville, Tel: 301 838 02 )
Fax: 301 838 02 /d
Fax: 301 838 02 /d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ996872 380
RPCI-23-383015.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shao, S., Nierman, W., Feldblyum, T., Malek, J., Shao, S., Levins, M., Mcyann, S., Tsegaye, G., Geer, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
1 (bases 1 to 380)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Fraser, C.M.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clones are derived itom the move of the following availability, please contact Pieter de Jong library availability, please contact Pieter de Jong (pieter@de)ong.med.buffalo.edu). Clones may be purchased from (pieter@de)ong.med.buffalo.edu)orderingframe.htm)
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from kesea ch Genetics (info@resgen.com). BAC end page:
or from kesea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse
                                                                                                                                                                                                                                                                                                                                                                            Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                        Plate:
                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.tigr.org/tdb/bac_ends/mouse/bac_end_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
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                                                                                                                                                                                                   /organism-"Mus musculus"
/strain-"C57BL/6J"
/db_xref-"taxon:10090"
/clone-"RPCI-23-383015"
/clone_lib="RPCI-23"
/sex="Female"
/note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or Brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI Sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                         1. .380
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Pred. No. 7.
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.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Jong, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Akinret
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ORIGIN

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Run
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_1101:*
1: /SIDS2/gcgdata
2: /SIDS2/gcgdata
3: /SIDS2/gcgdata
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114: ...

115: ...

116: ...

119: ...

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| SIDSZ/gcgdata/geneseq/yeneseqn/Na198.DAT:*
| SIDSZ/gcgdata/geneseq/yeneseqn/Na199.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqn/Na199.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            930621 segs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccagttctcaaaggagcagg
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/SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search time 578.64 Seconds (without alignments)
29.632 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Query Match Length DB	1	JD	Description
1	20	100.0	20	19	AAV31983	Human Down syndron
2	20	100.0	6413	19	AAV31988	Human Down
انيا	20	100.0	6604	19	AAV31981	Human Down
4	18.4	92.0	2173	19	AAV31987	Mouse Down
ر ت	18.4	92.0	54548	21	AAZ45596	DNA sequen
с 6	17.4	87.0	2197	21	AAZ89617	A. sydowi
c 7	16.8	84.0	187	16	AAT22739	Human gene signatu
c 8	16.4	82.0	12923	10	AAN90338	Sequence o
ი დ	15.8	79.0	209	22	AAI25968	Probe #159
c 10	15.8	79.0	209	22	AA153359	Probe #220
ဂ 11	15.8	79.0	563	22	AAI16773	Probe #670

New isolated hown's Syndrome-cell adhesion molecule develop products for detection, diagnosis and therapy  $\frac{1}{2} \left( \frac{1}{2} \right) \left( \frac{1}{2} \right)$ 

used ç WPI; 1998-271791/24.

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45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	լ u	12
15.2							15.2			15.2									15.2		15.4	15.4			15.4			Ģ				15.8	15.8
76.0	76.0	76.0	76.0	76.0	76.0	•		76.0	•			76.0			76.0	76.0	76.0	76.0	76.0	76.0	77.0	77.0	77.0		77.0	79.0	9		9	9	9	79.0	9
2652	2336	2303	1996	1930	1881	1881	1408	1407	1402	1229	1228	1209	892	798	750	478	351	180	167	47	4949	4646	1665	796	530	5406	2947	1972	1972	673	564	564	563
21	22	22	22	22	22	22	21	22	21	20	20	20	21	22	22	22	21	22	2.2	21	21	20	22	22	22	19	22	22	22	22	22	22	22
AAA61272	AAH16558	AAF30955	AAH15280	AAS22881	AAF27735	AAS22645	AAC43700	AAH42469	AAA96896	AAX81464	AAX81465	AAX81466	AAA49173	AAI 57849	AA159635	AA138475	AAC74771	AA151608	AAH09066	AAZ68502	AAC76989	AAX20577	AAH14284	AAH05981	AAH13400	AAV52299	AAH18697	AAI03989	AAI35523	AAH00627	AA108987	AAI48672	AAI40280
Human secreted pro	CUNA Sequ		_		Cran		Zea mays DNA tragm	Nucleotide sequenc	Nucleotide sequenc	Mosaic flaA gene c		flan gene	ncoding hu	Human polynucieoti	Human polynucieoti	Probe #/161 used C		Probe #20294 used		Human map-related	Human ORFX ORF2544	Polynucleotide seq	Human cDNA sequenc	Human cDNA clone (		Streptococcus pneu	Human cDNA sequenc	Probe #3980 used t	used	Enterococcus avium	Probe #8978 used t	Probe #17358 used	

## ALIGNMENTS

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RESULT
AAV31983
DS-CAM1; hown syndrome cell adhesion molecule; neural cell; signal transduction; trisomy 21; mental retardation; holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; human; PCR; primer; SS.
                                                                                                                                                                                                                                           Human Down syndrome-cell adhesion molecule DS-CAM primer B9-131F
                                                                                                                                                                                                                                                                                    AAV31983;
                                                                                                                                                                                                                                                                                                      AAV31983 standard; cDNA; 20 BP.
                                                                                                       23-OCT-1997;
                                                                                                                           30-APR-1998.
                                                                                                                                             W09817795-A1
                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                28-SEP-1998 (first entry)
                                              Korenberg JR,
                                                                                    25-OCT-1996;
                                                                                                                                                                Homo sapiens.
                                                                  (CEDA-) CEDARS SINAI MEDICAL CENT
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                                                                                   96US-0029322
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RESULT
AAV31988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forward primer B9-131F and reverse primer B9-131R (see AAV31984) were used in RT-PCR assays of cDNA libraries of various human tissues to determine human Down syndrome-cell adhesion molecule DS-CAM (see AAV31981 and AAV31988) expression. The results demonstrated expression of human DS-CAM mRNA in foetal and adult brain, and foetal kidney. In addition, a breast carcinoma cell line showed expression of human DS-CAM mRNA. DS-CAM polypeptides (see AAW42086-87) are associated with developmental and neurological processes. The polypeptides and nucleic acids are used to developmental products for the detection, diagnosis and therapy of developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental and neurological abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 79; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and neurological abnormalities
Whis cDNA clone codes for Down syndrome-cell adhesion molecule DS-CAM2 (see AAW42087), an extracellular, soluble protein belonging to a novel subclass of the 1g superfamily with highest homology to
                                                                                                                                                                                                                                                                                                                                                                                                                               holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; human; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DS-CAM2; Down syndrome-cell adhesion molecule; neural cell; signal transduction; trisomy 21; mental retardation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Down syndrome-cell adhesion molecule DS-CAM2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV31988 standard;
                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV31988;
                                                                                                                                                                                                                                                                                               30-APR-1998
                                                                                                                                                                                                                                                                                                                         ₩09817795-A1
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1998 (first entry)
                                                                                      New isolated Down's Syndrome-cell adhesion molecule - used to develop products for detection, diagnosis and therapy of developmental and neurological abnormalities
                                                                                                                                              WPI; 1998-271791/24.
P-PSDB; AAW42087.
                                                                                                                                                                                     Korenberg
                                                                                                                                                                                                                                                                     23-OCT-1997;
                                                             Claim
                                                                                                                                                                                                              (CEDA-) CEDARS SINAI MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100
les 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 BP; 6 A; 5 C; 6 G; 3 T; 0 other;
                                                               83-90;
                                                                                                                                                                                                                                          9608-0029322
                                                                                                                                                                                                                                                                     97WO-US19547.
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 6413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                               109pp;
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                                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DH 19; Length 20;
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RESULT
AAV31981
ID AAV3
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trapping, and the complete DS-CAM2 cDNA sequence was identified. DS-CAM2 is a splice variant of membrane-bound DS-CAM1 (see AAW42086) and is deleted for the entire transmembrane domain. The DS-CAM gene spans 900-1200 kb of genomic DNA and maps at chromosome 21q22-2-22.3. The invention also provides murine DS-CAM partial sequences (see AAV31985-87), expression vectors and host cells, sequences (see AAV31985-87), expression vectors and primers useful transgenic animals, autisense oilgonucleotides, and primers useful for amplification of DS-CAM nucleic acid. DS-CAM polypeptides are associated with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (reqenerating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and the products can also be used in detection, diagnosis and the products can also be used in detection, diagnosis and the products can also be used in detection, diagnosis and the products can also be used in detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neural cell adhesjon molecules. A modified direct cDNA selection technique was applied to bacterial and pl artificial chromosomes between ETS2 and MX1 by using cDNA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk constitution).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy of developmental and neurological abnormalities such as 
bown syndrome, mental retardation, holoprosencephaly, agenesis of 
the corpus callosum, or schizencephaly. Antisense oligonucleoti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gestation) cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4877 ccayttctcaaaygagcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6414 BP; 1633 A; 1781 C; 1707 G; 1292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DS-CAMI; bown syndrome-coll adhesion molecule; neural cell; signal transduction; trisomy 21; mental retardation;
                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                 schizencephaly; diagnosis; assay: human;
                                                                                                                                                                                                                                                                                                                                                                                                                              holoprosencephaly; corpus callean...denesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Down syndrome-cell adhesion molecule DS-CAM1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV31981 standard;
                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                  23-OCT-1997;
                                                                                                                                                                                                        WO9817/95-A1
                                                                (CEDA-) CEDARS
                                                                                                   25-OCT-1996;
                                                                                                                                                                       30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ccaqttctcaaaggagcagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                  SINAI MEDICAL CENT
                                                                                                   96US-0029322
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                                                                                                                                                                                                                                         /*tag- b
522..6162
/*tag- c
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453..6185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense oligonucleotides
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0;

WPI; 1998-271791/24

Korenberg

P-PSDB; AAW42086

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This cDNA clone codes for Down syndrome-cell adhesion molecule DS-CAMI (see AAW42086), a cell surface glycoprotein belonging to novel subclass of the Ig superfamily with highest homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4877 ccagiteteaaaggageagg 4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 65-72; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developmental and neurological abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Down's Syndrome-cell adhesion molecule - us develop products for detection, diagnosis and therapy of
                                                                                                                                                                                                                                                                                                                                                                                                              DS-CAM; Down syndrome-cell adhesion molecule; neural cell; signal transduction; trisomy 21; mental retardation; holoprosencephal; corpus callosum agenesis; schizencephaly; diagnosis; assay; mouse; ds; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6604 BP; 1673 A; 1827 C; 1768 G; 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV31987 standard; cDNA; 2173
                          (CEDA-) CEDARS SINAI MEDICAL CENT
                                                                                                                                                                                                                                                                                      W09817795-A1
                                                                                                                                                                                                                                                                                                                                                     Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse Down syndrome-cell adhesion molecule DS-CAM 3' cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-1998
                                                                                                                                                             23-OCT-1997;
                                                                                                                                                                                                                         30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ccagt teteaaaggageagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used for inhibiting translation of mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                             96US-0029322
                                                                                                                                                          97WO-US19547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -<u>-</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT
AAZ45596
                                                                                                                             δõ
                                                                                          В
                                                                                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   member of a novel subclass of the Ig superfamily with homology to neural cell adhesion molecules. The middle region (see AAV31986) and 5 region see AAV31985) of the clone are also provided. The murine DS-CAM clone was isolated from a C57 Black/6 mouse brain cDNA library using huma. DS-CAM cDNA (see AAV31981 and AAV31988) aprobe. The invention also provides human DS-CAM proteins (see
                                                                                                                                                                                                                                                                                                                                                                    associated with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (regenerating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                 Down syndrome, mental retardation, holoprosencephaly, agenesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic animals, antisense oligonucleotides, and primers useful for amplification of DS-CAM nucleic acids. DS-CAM polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe. The invention also provides numerican process.

AAW42086-87), as well as expression vectors and host cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             develop products for detection, diagnosis and therapy developmental and neurological abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-271791/24
                                                                                                                                                                                                                                                              Sequence 217 + BP;
                                                                                                                                                                                                                                                                                               are used for inhibiting translation of mRNA.
                                                                                                                                                                                                                                                                                                                                                    therapy of developmental and neurological abnormalities such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Down's Syndrome-cell adhesion molecule
AAZ45596 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for murine Down syndrome-cell adhesion molecule (DS-CAM), a
                                                                                          479 ccagttctccaaggagcagu
                                                                                                         1 ccaqttctcaaaqqagcaqq
                                   ر
ت
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequence comprises the 3' region of a cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Page 81-83; 109pp; English
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                585 A; 598 C;
                                                                                                                                                                                    92.0%;
95.0%;
 54548
                                                                                                                               20
                                                                                                                                                                    0;
                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                       Score 18.4;
                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                554 G; 436 T;
                                                                                                                                                                                        14;
                                                                                                                                                                                                       DB 19;
                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                    Ξ.
                                                                                                                                                                                                         Length
                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to
                                                                                                                                                                                                           2173;
                                                                                                                                                                                                                                                                                                                                                                                                                                  They can
                                                                                                                                                                    0;
                                                                                                                                                                    Gaps
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Human; PCTG4 region; X chromosome; q13 region; polymorphism; mental retardation; autism; depression; bipolar affective disorder; hypothyroidism; OPA gene; neuropsychiatric disorder; ss.
                                                                                                                                                                                                                       DNA sequence of the wild type human PCTG4 region of Xglf.
                                                                                                                                                                                                                                          06-APR-2000
                                                                                                                                                                                                                                                              AAZ45596;
                              exon
                                                                                                                                                             Homo sapiens
                                                          promoter
                                                                                        promoter
                                                                                                                                                                                                                                          (titst outry)
                                                        complement (1565..1815)
                                                                                      /number- |
/note= "human OPA
1398..1648
                                                                    /*tag= b
/note= "human
                  /*tag=
                             2008..2112
                                                                                                                                1391..1490
                                                                                                                                         Location/Qualifiers
/note= "human OPA promoter"
          /maber-
                                      /note- "unknown promoter"
                                                /*tag=
                                                  a
                                                                   OPA promoter"
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F 17 17 1	H H H H .	F F F F F	7777	7 7 7 7	1 1 1 1 1 1 1 1 1 1 1 1	)	F T T T	Ŧ Ŧ Ŧ Ŧ	n n n n	F F F F	13333	11 11 12	F T T T	F T T T	1 7 7 7 7	FT	FT FT
exon	exon	exon	exon	exon	exon	uoxe.	exon	exon	exon	exon	exon	exon	exon	exon	exon	exon	exon
io	97	/"Lag- L /number= 18 /note= "human OPA promoter" 89799122 /*tag= u	r.	F.	/"cag" q /number= 15 /note= "human OPA promoter" 7989.133 /*tag= r	77	/*tag- o /number= 13 /note= "human OPA promoter" 74037483	/*tag n /number 12 /notte "human OPA promoter" 67987027	/*tag= m /number= 11 /notte= "human OPA promoter" 62336359	/*tag= 1 /number= 10 /notte= "human OPA promoter" 57345865	/"tag" K /number= 9 /number= 9 /note= "human OPA promoter" 53775513	/*tag= j /number= 8 /notte= "human OPA promoter" 5148.5247	<pre>/*tag* i /number= 7 /norte= "human OPA promoter" 48394986</pre>	/*Eag* n /number* 6 /note* "human OPA promoter" 41974451	/*tag= g /number= 5 /note= "human OPA promoter" 39624072	<pre>/*tag* f /number* 4 /notte= "human OPA promoter" 36083787</pre>	/*tag= e /number= 3 /notte= "human OPA promoter" 26492805
FT exon	FT exon	FT exon	FT exon	FT exon	FT exon	FT FT exon	FT exon	FT exon	FT exon	FT FT exon FT	ET exon	FT exon	FT exon	FT exon	FT exon	FT exon	FT exon
/note= 20207. /*tag=	/note= "huma /note= "huma 198320029 /*tag= an /number= 38	/number= 30 /note= "huma 1952519675 /*tag= am /number= 37	/note= "huma 1892719301 /*tag= al	/note- "human 1773617897 /*tag= ak	/note= "huma 17351.17492 *tag= aj /number= 34	/number= 32 /note= "huma 1699917109 /*tag= ai	/number+ 31 /note= "huma 1576515854 /*tag= ah	/number- 30 /note= "human 1548715598 /*tag= ag	/number= 29 /note- "human 1501415175 /*tag= af	/number= 28 /note= "human 1471014843 /*tag= ae	/number= 2/ /note= "human 14187 .14258 /*tag= ad	/number= 26 /note= "huma 1267212851 /*tag= ac	/number= 25 /note= "human 1231712492 /*tag= ab	/number~ 24 /note= "huma 1175112065 /*tag= aa	/number~ 23 /note= "huma 1123511355 /*tag- z	/number= 22 /note= "huma 1093311077 /*tag= y	/number= 21 /note= "human 1053010757 /*tag= x

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AAZ89617/c
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
Matches 1
                                                                                                                                                                                                                                                                                                                      28196 ccagttcttaaaggagcagg 28215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                   promoter
Novel DNA encoding Aspergillus fructosyl transferase useful for production of polyfructose which is used to manufacture surfacts suspension agents .
                                                                                                                                                                                         Aspergillus sydowi.
                                                                                                                                                                                                           Fructosyl transferase; af1-SST;
viscosity; sedimentation; food;
                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                    DE19840028-A1
                                                                                                                                                                                                          viscosity;

    A. sydowi

                                                                                                                                                                                                                                                23-JUN-2000
                                                                                                                                                                                                                                                                AAZ89617;
                                                                                                                                                                                                                                                                                AAZ89617 standard;
                                WP1; 2000-257741/23
P-PSDB; AAY51947.
                                                                                       02-SEP-1998;
                                                                                                      02-SEP-1998;
                                                                                                                                                                                                                                                                                                                               1 ccagttctcaaaqgagcagg 20
                                                                                                                                                                                                                                                                                                                                                                     Match
                                                       ۶
                                                                                                                                                                                                                                                                                                                                                      l Similarity
19; Conser
                                                                       MAX PLANCK
                                                                                                                                                                                                                                  af1-SST cDNA
                                                        Rehm J,
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           /note= "human (
26123..26275
/*tag= au
                                                                                       98DE-1040028
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/note= "human
20372..20590
                                                                                                       98DE-1040028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "human
23283..23505
                                                                                                                                                   /*rag= a
/product= "afl-SST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24531..24612
                                                                                                                                                                   21..2069
                                                                                                                                                                                                                                                                                                                                                                                     /note= "probable NL-3 promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                   24823..25096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note≈ "human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=
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                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         '*tag≖
                                                                        GES FOERDERUNG
                                                                                                                                                                                                                                                                                 cDNA; 2197
                                                        Wendenburg
                                                                                                                                                                                                                                                                                                                                                             92.0%;
95.0%;
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r= 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39
                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                      Score 18.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPA
                                                                                                                                                                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                            OPA promoter"
                                                                                                                                                                                                           polyfructose; surfactant manufacture;
ss.
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         promoter"
                                                                         WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                              No. 19;
          to manufacture surfactants
                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                       1.
                                                                                                                                                                                                                                                                                                                                                                      Length 54548;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                        0;
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          and
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AAT22739/c
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel nucleic acid molecule (I) encoding a fructosyl transferase isolated from Aspergillus sydowi. The fructosyl transferase is useful for the production of polyfructose. Polyfructose can be used to manufacture surfactants, to increase the viscosity of an aqueous system, as a suspending agent, to accelerate sedimentation and in the formation of complexes or to bind water. The host cell can be used as a food. This sequence encodes the A. sydowi fructosyl transferase designated aff-SST which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1b; Page 12-15; 28pp;
                                                                                                                                                                                                                                                                                                                                                                                                  AAT22739 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2197
                                                                                                                                                                                                                                                                                                                                                                                                                                            728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 515 A; 587 C; 575 G; 520 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.0%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                  to mRNA; 187 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                            710
                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.4;
No. 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Gene sign ture; messenge human; clening; mapping;
                                                                                                                                                                           01-JUN-1995
                                                                                                                                                                                                                                                                                                                                    Human gen · signature HUMGS04398
                                                                                                                                                                                                         W09514772-A1
                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                      cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1996
WPI; 1995-206931/27.
                              Matsubara K,
                                                                                                             12-NOV-1993;
                                                                                                                                           11-NOV-1994;
                                                            (OKUH/)
                                                                             MATS/)
                                                              OKUBO
                                                                             MATSUBARA
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                              Okubo
                                                                                                             9301-035504
                                                                                                                                             94MO-JP01916
                                                                                                                                                                                                                                                                                                         messenger
                                                                                                                                                                                                                                                                                      non-biased library; diagnosis;
                                                                                                                                                                                                                                                                                                         relative abundance; frequency;
                                                                                                                                                                                                                                                                                           detection;
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 \*GS\* sequences given in AAR19001-726837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.

Claim 1; Page 1203; 2245pp; Japanese

Identifying gene signatures in 3'-direct for diagnosis of abnormal cell function, reflects relative abundance of corresp.

3'-directed human cDNA library -function, by preparing cDNA that corresp. mRNA in specific human

e.g.

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SSSSSS
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I/ AAN90338 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
                                   Query Match
Best Local
                          Martches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                           The inventors claim an MD probe comprising a purified ss NA:50 which hybridises to at least a part of the MD gene; pure dystrophin (DS) polypeptide, purified NA encoding DS and antibodies (Ab) to DS. The probes are equal to or greater than 10b of one of 12 cDNA sequences deposited as ATCC 58666-57677. The MD gene is human, or a murine Dmd deposited as ATCC 58666-57677.
                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 187 BP; 48 A; 42 C; 42 G; 49 T;
                                                                                                                                                                                                              Muscular dystrophy gene - used for prepn. of probes, dystrophin polypeptide and antibodies for diagnosis and therapy of muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dystrophin; muscular dystrophy; probe;
prenatal; heterozygote; gene therapy; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of human muscular dystrophy (MD) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAN90338;
                                                                              Sequence 12923 BP;
                                                                                                                                                                               Disclosure; Fig 5; 68pp; English
                                                                                                                                                                                                     dystrophy
                                                                                                                                                                                                                                               WPI; 1989-220587/30.
P-PSDB; AAP90373.
                                                                                                                                                                                                                                                                                                                          22-DEC-1987;
                                                                                                                                                                                                                                                                                                                                               16-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                     13-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                           W08906286-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             foetal screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-1992
                                                                                                    gene.
                                                                                                                                                                                                                                                                                                    (CHIL-) CHILDRENS MED CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
                        Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ccagttctcaaaggagcagg
cagtictcaaaggagcag 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heterozygote; gene reening; ss.
                          Conservative
                                                                                                                                                                                                                                                                               Monaco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                          87US-0136618
                                                                                                                                                                                                                                                                                                                                                88WO-US04504
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 209..12923
                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA; 12923
                                                                               4296 A; 2613 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.0%;
90.0%;
                                    82.0%;
                                                                                                                                                                                                                                                                                 Hoffman
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                          0;
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Pred.
                                    Score 16.4;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                 ΕP,
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                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
                                                                               2963 G;
                                                                                                                                                                                                                                                                               Koenig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8;
64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; diagnosis;
                         1.5e+02;
1;
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                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                3044 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                              Length 12923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 187;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                7 other;
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                           0
                           Gaps
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RESULT 9
AAI25968/c
RESULT 10
AAI53359/c
ID AAI533
XX
AC AAI533
XX
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Best Local S
Matches 17
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30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO as for a part of the printed as the problem of the printed as the printed as the problem of the problem o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; human; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe #15901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001
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                  AAI53359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID No 15901; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                  AAI53359 standard; DNA; 209
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 209 BP; 47 A; 59 C; 54 G; 49 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                            1 ccagttctcaaaggagcag
                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                     l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000US-0180312
2000US-0207456
; 2000US-0608408
; 2000US-0632366
; 2000US-0632366
; 2000US-0234587
; 2000US-0236559
; 2000US-0236559
; 2000US-0236559
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                          79.0%;
89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11887
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                                                                  Bp
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                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                   Score 15.8; DB 2:
Pred. No. 1.9e+02
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
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                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epithelial cell;
                                                                                                                                                                                                                                                                                                                    209;
                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                        Gaps
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0

17-OCT-2001 (first entry)

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Query Match
Best Local Similarity 89.
Matches 17; Conservative
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID No 22045; 654pp;
                                                                                                                                                                                                                                                                                                                                                                                                   analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000;
                                                                                                                                                                                                                                                                                                        Sequence 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                   cervical
                                                                                            Probe;
                                                                                                                Probe #6706 for gene expression
                                                                                                                                                   AAI16773;
                                                                                                                                                                       AAI16773 standard;
           30-JAN-2001; 2001WO-US00670
                             09-AUG-2001
                                                WO200157278-A2
                                                                                                                                  12-OCT-2001
                                                                                                                                                                                                                     175
                                                                  Homo sapiens
                                                                                                                                                                                                                             ccagttctcaaaggagcag 19
                                                                                                                                                                                                                                                                                                                                                                                                                               2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #22045 used
                                                                                                                                                                                                                     CCGGGTCTCAAAGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful zing gene expression in human placenta .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarray;
                                                                                   human; microarray;
al cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US00663
                                                                                                                                                                                                                                                                                                         BP; 47 A; 59 C;
                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to measure gene expression in human placenta sample
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                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                    79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen
                                                                                                                                                                         563
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                                                                                              gene
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                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                    Score 15.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                          54 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR
                                                                                               expression; cervical epithelial cell;
                                                                                                                 analysis in uman cervical cell sample
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antenatal diagnosis;
                                                                                                                                                                                                                                                                                                           T; 0 other;
                                                                                                                                                                                                                                                           ..9e+02;
2;
                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                209;
                                                                                                                                                                                                                                                                                                                                                          probes (SENP).
                                                                                                                                                                                                                                                                                                                                                                                                                 for
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                                                                                                                                                                                                                                                                                                                                       lng gene
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В
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                                                                                                                                                                                                                                                                                                                                         RESULT 12
AAI40280/c
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Best Local Similarity
Matches 17; Conserv
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26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire with from the country and the country and the country are considered.
                                04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human geno
analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 563
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                       genetic
                                                                                                                                                                                                                                                        Probe #8966
                                                                                                                                                                                                                                                                                                       AAI40280;
                                                                                                                                                                                                                                                                                                                             AAI40280 standard;
                                                                                                                             30-JAN-2001;
                                                                                                                                                   09-AUG-2001
                                                                                                                                                                         WO200157272-A2
                                                                                                                                                                                                                                  Probe; microarray;
                                                                                                                                                                                                                                                                                17-0CT-2001
         (MOLE-) MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                      326 CCGGGTCT: AAAGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                  1 ccagttctcaaaggagc ; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells
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                                                                                                                                                                                                                       disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID No 6706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-02368359.
                                                                                                                                                                                                                                                          used to
                                2000US-0180312
2000US-0207456
2000US-0698408
2000US-0698408
2000US-0632366
2000US-0234687
2000US-0236359
2000US-0236353
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           вр; 115 A;
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                             2001WO-US00663
                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                     human;
                                                                                                                                                                                                                                                        measure gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153
                                                                                                                                                                                                                                                                                                                               563
                                                                                                                                                                                                                                                                                                                                                                                        308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                487pp; English.
                                                                                                                                                                                                                                   placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 178
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                                                                                                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.8;
No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR;
                                                                                                                                                                                                                                   antenatal
                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                      diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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RESULT 13
AA1486
XX AA1486
XX Probe
XX O9-AU
XX 04-FE
PR 30-JU
PR 30-JU
PR 31-SE
PR 04-GC
XX PPI
XX The F
CC TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
-26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #17358 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI48672 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157272-A2
                    The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326
                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid analyzing gene expression in human placenta .
                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ccagttctcaaaggagcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
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17; Conserv
                                                                                                                                                                                                                                                                                              2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel
                                                                                                                                                                          SEQ
                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-068408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236263.
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                                                                                                                                                                             dI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No 8966; 654pp; English
                                                                                                                                                                             o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to measure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen
                                                                                                                                                                                                                                                                                                                                               Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308
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                                                                                                                                                                                                                                                                                                                                                  ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                               654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.8; DB 22; pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                     Rank
                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                     DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes
                                                                                                                                                                                                                                                     probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sample
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Query Match Best Local S Matches 17

l Similarity 17; Conserv

Conservative

79.0%;

Score 15.8; DB 22 Pred. No. 2.1e+02; 0; Mismatches 2

22;

Length Indels

0

Gaps

0

Sequence

564

B₽;

137

Α,

149 C;

139 G;

139 T;

0

other;

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RESULT 14
AAI08987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 564 HP; 137
                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA108987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI08987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe; human; breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe #8978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ccagttctcaaaggagcag
                                                           The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast particularly those diseases with polygenic aeticlogy. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and prognosing contractions.
                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory
                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2001;
                                                                                                                                                                        Claim 25; SEQ ID NO 8978; 322pp; English
                                                                                                                                                                                                        Novel
                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                               WPI; 2001-476286/51
                                                                                                                                                                                                                                                                         (MOLE-)
                                                    of the breast, fibrocystic non-carcinoma tumours
                                                                                                                                                                                                in a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                      SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
17; Conserv
                                                                                                                                                                                                          single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                           MOLECULAR DYNAI
                                                                                                                                                                                                                                                      Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used
                                                                                                                                                                                                  breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to
                                                                                                                                                                                                                                                      DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        measure
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89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                        Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          뜓
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                                                                                                                                                                                                             probe used to
                                                                                                                                                                                                                                                         Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22
.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Η.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast
                                                                                                                                                                                                                gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564;
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                                                                                                                                       the probe
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AAH00627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium sp., Enterobacteriaceae group, Escherichia coll, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Weisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 24; Page 763; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bergeron MG, Bozsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species specific; genus specific; family specific; probe; detection identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-245006/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-1999; 99CA-2283458
19-MAY-2000; 2000CA-2307010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catalytic subunit of proton-translocating ATPase; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus avium nucleotide sequence SEQ ID NO:618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH00627 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-2000; 2000WO-CA01150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200123604-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus avium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH00627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boissinot M, Huletsky A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouellette
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Sequence 673

BP;

210 A;

120 C;

154 G; 189

T; 0 other;

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Qy
   В
                                  Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
223
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Pred. No. 2.1e+02;
                                  Mismatches
                                                   DB 22;
                                                 Length 673;
                                  Indels
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Search completed: March 4, 2002, 05:21:23 Job time: 17512 sec

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OM nucleic .

nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

March 4, 2002, 05:11:29;

Search time 226.99 Seconds (without alignments) 19.955 Million cell updates/sec

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Sequence 26, Appl
Sequence 49, Appl
Sequence 51, Appl
Sequence 53, Appl
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1, Appli
313, App
      2. Appli
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1, Appli
2, Appli
                                                                                                                                                                                                            App.
                                                                                               TELEFAX: 201-994-1744

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
HENGTH: 3417 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
US-08-464-402-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-464-402-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
ZIP: 07068
COMPUTER READDABLE FORM:
COMPUTER READDABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10 MAK 95

FILLING DATE: 11 MAK 95

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 35.134

REGISTRATION NUMBER: 325800-388

REFERENCE/DOCKET NUMBER: 325800-388

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
                             Matches
                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WEI, ET AL.
TITLE OF INVENTION: Hur
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: UFILING DATE: June 5, CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
14
14
14
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14
1 ccagttctcaaaggagcagg 20
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                             1 Similarity 85.0
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4821
5925
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5925
10299
10299
10299
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                                                76.0%;
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US-08-470-260-4
US-08-471-491-4
US-08-477-451-1
US-08-477-451-5
US-08-477-451-25
US-08-477-451-25
US-08-477-278-1
US-08-272-255-19
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US-08-850-119-2
US-08-850-119-2
US-08-850-119-2
US-08-461-697-396
US-09-461-697-396
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                                   Score 15.2; D
pred. No. 71;
0; Mismatches
                                     0
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                                                                    DB 2;
                                                                    Length 3417;
                                             Indels
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Sequence
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40, Appl

10, Appl

11, Appl

19, Appl

19, Appl

20, Appl

410, Appl

21, Appl
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Minimum DB s Maximum DB s

seq

length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_NA:\*
1: /cgn2\_6/ptodata/2/
2: /cgn2\_6/ptodata/2/
3: /cgn2\_6/ptodata///

/cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
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/cgn2\_6/ptodata/2/ina/BCTUS\_C.MB.seq:\*
/cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

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14.8 14.8 14.8 14.4 14.4 14.4 14.4 14.4

1785 11977 11977 2071 8535 92071 1314 1875 2135 3648 3648 3648 3648 4821 4821 4821

Sequence Sequence Sequence Sequence Sequence

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US-08-464-402-1
US-09-054-775C-1
US-09-057-049-1
PCT-US93-03076-1
US-08-459-146-1
US-08-459-065-1
US-09-234-393-51
US-09-234-393-51
US-09-234-393-53
US-09-234-393-23
US-09-234-393-23
US-09-235-373-2
US-08-258-373-2
US-08-53-614-1
US-08-258-373-1
US-08-258-373-1
US-08-316-3978-3
US-08-316-3978-3
US-08-053-614-3

Sequence Sequence Sequence

Sequence

14 15 16 17 18 19 20 20 21 22 23 24 25 25

No

Query Match

Length DB

Description Sequence

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76. 76. 76. 76. 76. 74. 74. 74. 74. 74.

Sequence Sequence Sequence Sequence Sequence Sequence

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched:

, number of

hits satisfying chosen parameters:

351203 seqs, 1:13238999 residues

Title: perfect score:

US-08-956-991-5 20 1 ccagttctcaaagg

ccagttctcaaaggagcagg

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US-09-054-775C-1
                                                                                                                                                                                          RESULT 3
US-09-187-049-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09054775C Patent No. 6284504 GENERAL INFORMATION:
                                                                                                                                            Sequence 1, Application US/09187049 Patent No. 6117666
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/054,775C
FILING DATE: 03-Apr-1998
APPLICATION NUMBER: US 08/464,402
APPLICATION NUMBER: BCT/US95/03939
FILING DATE: 31-AMR-1995
APPLICATION NUMBER: PCT/US95/03939
FILING DATE: 31-AMR-1995
APPLICATION NUMBER: H0,302
RESEISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF161D1
RESEISTRATION NUMBER: PF161D1
                                                                                                                                                                                                                                                                             2559 CCAGTTGTCCAAGGAGAAGG 2578
                NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                         TITLE OF INVENTION: PLASTID PROTEOLYTIC PROCESSING ENZYME TITLE OF INVENTION: THAT CLEAVES PRECURSOR POLYPEPTIDES
                                                                                                       APPLICANT: Lamppa, Gayle K.
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                     1 ccagttctcaaaggagcagg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haseltine, William TITLE OF INVENTION: Human DNA Ligase III NUMBER \cap F SEQUENCES: 10
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wei, Ying-Fei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3417 base pairs
                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                     Conservative
BRINKS HOFER GILSON & LIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                   76.0%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                     0;
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pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 3417;
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TELECOMNUM...

TELEPAX: 312 321-4299

TELEFAX: 312 321-4299

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4337 base pairs

TYPE: nucleic acid

TYPE: nucleic single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: CDNA US-09-187-049-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US93-03076-1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application PC/TUS9303076
GENERAL INFORMATION:
APPLICANT: whitehead Institute for Biomedical Research
TITLE OF INVENTION: GAP-Associated Protein pl90 and
TITLE OF INVENTION: Transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MAILIN, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1170RWATION:
TELECOMMUNICATION 123-4200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2567 CAACTTCTCAAGGGAGCAGG 2586
                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia.
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH192-03A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. E
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/187,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                     STREET: 2 Milit. CITY: Lexington
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                                                                                                                               APPLICATION NUMBER: FILING DATE: 19930:
                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application PC/TUS9303076
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                                                                                                                                 19930331
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85.0%;
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pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:

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; NAME/KEY:
; LOCATION:
PCT-US93-03076-1
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; STRAIN: US-08-459-146-1
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                               TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12752 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Genetically Engineered Transmissible TITLE OF INVENTION: Hypovirulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 851
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                              ORIGINAL SOURCE:
ORGANISM: End
ORGANISM: par
                                                                                       MOLECULE TYPE: CI
                                                                            ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/459,146
FILING DATE: 02-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Nutley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                   EP713
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731..5272
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                                                                               N<sub>O</sub>
                               Endothia parasitica (Cryphonectria parasitica)
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85.0%;
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Pred. No. 82;
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US-08-459-065-1
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Patent No. 5882642
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Best Local Similarity
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                                                             Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12752 hase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-105/MS-UOS
SOFTMARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION UNIVERSE. 1267087459 065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically En
TITLE OF INVENTION: Hypovirulence
12192 CCAACTCGCAAAGGAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,117
FILING DATE: 06-FEH-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROSeman, Catherine R
REGISTRATION NUMBER: 34,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
                                                                                                                                                                                               HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                               ORGANISM: Endothia parasitica (Cryphonectria ORGANISM: parasitica)
                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 8589
                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                   1 ccagttctcaaaggagcagg
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                                                             Conservative
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                                                                                                                                                                                                                                                              Linear
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85.0%;
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Pred. No. 8
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                                                                            Score 15.2;
Pred. No. 88;
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RESULT

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APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
"URRENT APPLICATION NUMBER: US/09/328,111
"REENT APPLICATION NUMBER: US/09/328,111
"REENT FILING DATE: 1999-06-08
AARLIER APPLICATION NUMBER: US 60/088,801
LARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 313
LENGTH: 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; LOCATION: (1)...(656)
; OTHER INFORMATION: n = A,T,C
US-09-328-111-313
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                                                                                      ; TYPE: DNA ; ORGANISM: Abies grandis US-09-234-393-26
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ent No. 6265639
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Best Local Similarity
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                                                                                                                                                                          SEQ IU NO 26
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
Query Match
Best Local Sjmilarity
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APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/234,393A CURRENT FILING DATE: 1999-01-20 EARLIER APPLICATION NUMBER: 60/072,204 EARLIER FILING DATE: 1998-01-22 NUMBER OF SEQ ID NOS: 55 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                         APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John E
APPLICANT: Bohlman, Jorg
APPLICANT: Jetter, Reinhard
APPLICANT: Steele, Christopher L
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: WSUR113345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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                                                                                                                                                     ENGTH:
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88.9%;
      74.0%;
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Pred. No. 85;
         Score 14.8;
Pred. No. 97;
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                             DB 4;
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APPLICANT: Croteau, Rodney H
APPLICANT: Croteau, Rodney H
APPLICANT: Crock, John E
APPLICANT: Bobliman, Jorg
APPLICANT: Jetter, Reinhard
APPLICANT: Jetter, Reinhard
APPLICANT: Jetter, Reinhard
APPLICANT: Jetter, Reinhard
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: WSUR113345
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT APPLICATION NUMBER: 60/072,204
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER SILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
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; LOCATION: (4)..(1782)
US-09-234-393-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-234-393-51
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Croteau, Rodney
APPLICANT: Crock, John E
                                                                              APPLICANT: Jetter, Reinhard
APPLICANT: Steele, Christopher I.
APPLICANT: Steele, Christopher I.
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: WSUKI13345
FULE REFERENCE: WSUKI13345
FULER APPLICATION UNMER: US/09/234,393A
CURRENT FILING DATE: 1994-01-20
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER APPLICATION NUMBER: 60/072,204
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 49, Appli
Patent No. 6265639
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51, Application 05/05/44/09A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.0%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bohlman, Jorg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: gamma humulene synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                  TYPE: DNA ORGANISM: Artificial Sequence
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FEATURE:
                                                            LENGTH: 1785
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; LOCATION: (4)..(1782)
US-09-234-393-51
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                           US-09-234-393-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Form
APPLICANT: Steele, John E
APPLICANT: Steele, Christopher L
APPLICANT: Steele, Christopher L
APPLICANT: Steele, Christopher L
APPLICANT: Steele, Christopher L
APPLICANT: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: MSUR113345
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
NUMBER OF SEG ID NOS: 55
           GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Crock, John E

APPLICANT: Bohlman, Jorg

APPLICANT: Jetter, Reinhard

APPLICANT: Steele, Christopher L

APPLICANT: Steele, Christopher L

TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIK (ABIES GRANDIS)

TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.0%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ratent No.
                                                                                                                                                                              Sequence 23, Appli
Patent No. 6265639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: gamma humulene synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quence 53, App. -
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LOCATION: (4)..(1782)
'9-234-393-53
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|1616 agttcttaaayaagcagg 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: computer-generated nucleic acid sequence encoding OTHER INFORMATION: gamma humulene synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                      REFERENCE: WSUR113345
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Pred. No. 1e+02;
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Pred. No. 1e+02;
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; NAME/KEY: CDS
; LOCATION: (4)..(1782)
US-09-234-393-23
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US-09-023-023-1/c
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LENGTH: 1977
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Patent No. 6121018
GENERAL INFORMATION:
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Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Abies grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
Best Local Similarity Matches 16; Conserv
                                   Query Match
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                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1616 agttcttaaagaagcagg 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kristine Kay Kikly
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis
RUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Heecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/0
FILING DATE: March 27, 1
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/023,023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READIBLE FORM:
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2071 base pairs
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COMPUTER: IBM Con
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                 NAME: Han, William T
REGISTRATION NUMBER:
                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                       TELEFAX: 610-270-5090
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                         Score 14.8; DB 3; Pred. No. 1e+02;
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                                           Length 2071;
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Mismatches

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Indels

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RESULT 14
US-08-716-351A-1
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CLASSIFICATION DATA:

APPLICATION NUMBER: PCT/US94/03784

FILING DATE: 06-APR-1994

ATTORNEY/AGENT INFORMATION:

INAME: BASTLAN, Kevin L.

REGISTRATION NUMBER: 34,774

REGISTRATION NUMBER: 15280-128-1PC

TELEFORMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-9600

TELEFAX: (415) 543-960

ITELEFAX: (415) 543-961

SEQUENCE CHARACTERISTICS:

LENGTH: 8535 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
APPLICANT: Fletcher, Jonathan A.

APPLICANT: Xiao, Sheng
TITLE OF INVENTION: HMGI(Y)-LAMA4* FUSION ONCOGENE,
TITLE OF INVENTION: ONCOPROTEIN AND METHODS OF USE
FILE REFERENCE: B0801/7135/ERP
CUBRENT APPLICATION NUMBER: US/09/258,373
CURRENT FILING DATE: 1999-02-26
EARLLER APPLICATION NUMBER: 60/076,401
EARLLER FILING DATE: 1998-02-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                         RESULT 15
US-09-258-373-2/c
; Sequence 2, Application US/09258373
; Patent No. 6150110
; GENERAL INFORMATION:
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St Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,351A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                            2 cagttctcaaaggagcag 19
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1977 CAGGTCTCAAAGJGGCAG 1994
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OTHER INFORMATION: /standard_name=
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Search completed: March 4, 2002, 05:11:33 Job time: 16947 sec

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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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No.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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16.8
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Match Length
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Gapop 10.0 , Gapext 1.0
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 BF348620
AZ297511
CNS0507U
BG700618
BG701055
BB373590
F25472
BB528026
BB367406
BE032419
BH604281
BB429902
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  HF348620 602019924
AZ297511 RPCI-23-1
AL315219 Tetraodon
BG700618 602682215
BG701055 602682072
BH373590 B0373590
F25472 HSD12539 H
BB528026 BB528026
BH367406 BH367406
HE032419 121758 MA
HB604281 HB604281
BB429902 BH429902
                                                                                                                                        Description
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## ALIGNMENTS

Source	FEATURES	TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BF348620 LOCUS DEFINITION
/organism="Homo sapiens" /dh_xref="taxon:9606" /clone="IMAGE:4155508" /clone_lib="McI_CGAP_Brn67" /tissne_type="anaplastic oligodendroglioma with lp/19q toss"		National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Liausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: David N. Louis, M.D.	Homo sapiens Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryola; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 744) NIH-MCC http://mqc.nci.nih.gov/.	5', mRNA sequence. BF348620 RE448620.1 GI:11296215 EST. human.	BF348620 744 bp mRNA EST 22-NOV-2000 602019924F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155508

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                                                                                                                                                                                                                                                                                                                                                                                                                                BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 117 row: G column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Other_GSSs: RPCI-23-117G10.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., dt. Jong, P
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Clones are derived from the mouse BAC library RPC1-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Dr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     library availability, please contact Pieter de Jong
(pieteredejong.med.buffalo.edu). (lones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301 838 0200
Fax: 301 838 0208
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Medical Center Dr., Rockville, MD 20850,
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/note="Organ: brain; Vector: pCMV-SPORR'6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 &b. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
196 c 210 g 150 t
                                                                                                       /note-*Organ: Kidney/Brain: Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoKI and EcoRI Methylase. Size
                  selected DNA was cloned into the pBACc3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Lite Technologies).
                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain~"C57BL/6J"
                                                                                                                                                                                               /lab_host="DH10B"
                                                                                                                                                                                                               /clone_lib="RPCI-23"
/sex="Female"
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/clone="RPCI-23-117G10"
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                                                                                                                                                        1 cctgtatgacctgcaggaa 19
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2 (bases 1 to 903)
2 (rollius, H.R., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
2 Bernot, A. and Weissenbach, J.
2 Characterization and repeat analysis of the compact genome of the freshwater pufferfish tetraodon nigroviridis
3 Genome Res. 10 (7), 939-949 (2000)
3 0 3 5 98 37
                                                                                                                                       CCTGAATGACCTGCAGGAA 87
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GSS; genome survey sequence.
GSS; genome igroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Aranthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a simple read and was generated as part of a large scale clone and sequencing project of the Tetraodon nigroviridis genome. For more intormation, please take a Jook at http://www.accuescope.cms.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetler,F.,
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19; Conservative
BG700618 559 bp mkNA EST 602682215F1 NIH_MGC_95 Homo sapiens cDNA clone mkNA sequence.
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1 (bases 1 to 903)
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                                                                                                                                                                                                                      Conservative
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/db_xref-"taxon:99883"
/clone="027C17"
                                                                                                                                                                                                                                                                                                                                     /clone_lib-"B"
/note="Genoscope sequence
/note="Genoscope sequence
/ 159 c 176 g 231
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Pred. No. 3.5e+02;
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                                                                                                                                                                                                                                       Score 17.4; DB 13
Pred. No. 9.5e+02;
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t 35 others
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                          TITLE
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                                                                                                                                                 JOURNAL.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The [.M.A.G.E. Consortium (LLNL)
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National institutes of Health, M
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BG700618.1 GI:13970140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://image.llnl.gov
Plate: LLAM10711 row:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                Unpublished (1999)
Contact: Kobert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 655)

NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BG701055
BG701055.1 GI:13971014
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                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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cDNA Library Preparation: Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 559)
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/db_xref="taxon:9606"
/clone="IMAGE:4815146"
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/lab_host="DH10B"
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    Brownstein (NHGRI), Shiraki
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RESULT
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                                                                                                               Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                   RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
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Tel: 81-45-503-9222 Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB373590.1 G1:9085684
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Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic
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/lab_host="DH10B"
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/clone_lib-"NIH_MGC_95"
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URL:http://genome.gsc.riken.go.jp/
Carninci.p., Nishiyama,r., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Carrinci, P. and Hayashizaki, Y.
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18; Conserv
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                                                                                                                                                                            EST
1 (bases 1 to 188)
Lanfranchi,G., Muraro,T., Caldara,F., 'acchioni,B., Pallav
Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
Identification of 4370 expressed sequence tags from a
                                                                                                                               Homo sapiens
                                                                                                                                                                                                F25472.1
                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Lissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
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/clone="C130071C07"
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/strain="C578L/6J"
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90.0%;
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                                                                                          RS Konno, H., Aizwa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci P., Endo, T., Fukud, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Hori, F., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shigata, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shipata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Watanabe, S., Yamamura, T., Yamanaka, I., T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Nakanabe, S., Yamamura, T., Yamanaka, I., Yamanaka, Yaman
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ABI Chromatograms and other information are available on WWW
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moscolos cDNA clear D930044H02 C similar LO M28383 MOUSE AE3 mRNA,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
                                                                       Contact: Yoshihide Hayashizaki
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/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
Site_2: Not1; The library was constructed by G.
Lantranchi. This library is not subtracted nor normalized.
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/db_xre: "taxon:9606"
/clone-:.4000038E11"
/clone_lib-"HM3"
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Pred. No. 1.6e+03;
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uRL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
v., Okazaki,Y., Muramatsu,M. and Hayashlzaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
v. and U.S. Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Tel: 81-45-503-9222
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Carninci,P. and Hayashizaki,Y.
                                                                                                       BB367406 274 bp mRNA EST 12-JUL-2000 BB367406 KIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone C130037M06 3' similar to AB025261 Sus scrofamRNA for myosin heavy chain 2b, mRNA sequence.
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                       house mouse.
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-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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81-45-503-9216
  musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mc use Genome Encyclopedia Project of Genome Exploration Research foroup in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="n930044H02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full length by
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/dev_stage="15 days embryo"
/lab_host="DH10B"
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Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sughiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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Mammalia; Eutheria;
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasa
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasa
Carninci,P., Nishiyama,J., Sasa
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes
trehalose and its application for the synthesis of full length
cDNA, Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
cDNA, Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Ttoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Okaza
Tomarn,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okaza
Y. and Hayashizaki,Y.
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303
19-44 (1999)
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Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                               prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
                                                                                            prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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/dev_stage-"16 days embryo"
/lab_host-"DH10B"
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/db_xret-"taxon:10090"
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                                                            modified pBluescript
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                                                               KS(+) after bulk excision
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|| 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 
                                                                                                                                                                                                                                                                                                            253 CCTGTATGAGCTGAAGGAAG 272
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 276)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
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131758 MARC 1PIG
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrota
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PO Bo
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Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 402 762 4366
Fax: 402 762 4390
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                                                                              BB604281 278 bp mRNA
BB604281 RIKEN tull-length enriched, 15 days embryo head Mus
musculus cDNA clone D930013C15 5', mRNA sequence.
BB604281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCCAGTCACGACG
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 64 row: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR PRimers
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EST.
house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Sus scrofa"
/db_xref="taxon:9823"
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90.0%;
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Pred. No. 1.7e+03;
0; Mismatches 2;
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Pred. No. 1.
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Sus.
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Query Match
Best Local Similarity
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

22 | (bases 1 to 278)

23 | (bases 1 to 278)

24 | Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P.

25 | Alzawa, K., Akahira, S., Akimura, T., Hirozane, T., Hodoyama, Y.,

26 | Hanagaki, T., Hayyatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y.,

27 | Inotani, K., Ishii, Y., Itoh, M., Izawa, M., Rawai, J., Kojima, Y., Konno

28 | Imotani, K., Ishii, Y., Itoh, M., Izawa, A., Rawai, J., Kojima, Y.,

29 | Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C.,

20 | Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C.,

20 | Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A.,

20 | Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Tanaka

20 | T., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K.,

21 | Yoshiki, A., Muramatasu, M. and Hayashizaki, Y.

22 | RIKEN Mouse ESTs (Aizawa, K. et al. 2000)

31 | Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-resegsc.riken.go.jp/
UKU:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Toharu,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, KIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An omated tiltration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carningi, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High-efficiency tull-length cDNA cloning.
                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Lissue_type-"head"
/dev_stage-"15 days embryo"
/lab_host-"DH108"
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/etone "p930013c15"
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                                                                                                                                                                                                                                                                                         cap-trapper. Second strand cDNA was prepared with primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                      prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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                                                                                                                                                                                                                               modified pBluescript KS(+) after
                                                                                                                                                                                                                                                              was cloned into the XhoI and BamHI sites.
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   84.0%;
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   Score 16.8; DB 10;
Pred. No. 1.7e+03;
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                                         Length 278;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci P., E., D., Fukuda, S., Fukunishi, , Hara, A., Hayatsu, N., P., E., Lo, T., Fukuda, S., Fukunishi, , Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kukuchi, N., Izawa, M., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M. Kiyosawa, H., Kojima, Y., Koya, S., Kurihara, C., Kusakabe, M. Kiyosawa, H., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Miki, R., Sato, K., Shibata, K., Shibata, Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, K., Shibata, Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, K., Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, Szzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Szzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Szzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Szzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Szzuki, H., Suzuki, H., Tagawa, A., Shiraki, T., Yoshida, K., Yoshiki, A., Yoshino, Yano, R., Yasuishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y., RIKEN Mouse ESTS (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cctgtatgacctgcaggaag
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BB429902 RIKEN full-length enriched, adult male hippocampus MU
musculus cDNA clone C630030M10 3' similar to M28383 Mouse AE3
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 291)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka.S., Sasaki
Carninci.P., Waramatsu,M. and Hayashizaki.Y.,
N., Okazaki.Y., Muramatsu,M. and Hayashizaki.Y.
N., Okazaki.Y., Muramatsu,M. and Hayashizaki.Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of the synthesis of full length
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Toh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci.P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                 further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High-efficiency full-length cDNA cloning.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="C630030M10"
                                                                                                                                                                                                                                                                                         /organism≖"Mus musculus"
/strain~"C57BL/6J"
                                                                                  /tissue_type="hippocampus"
/dev_stage="adult"
                                                                                                                                                                                                       /clone_lib-"RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
/note="Site_1: Xho1: Site_2: HamH1; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                            /lab_host-"SOLR"
                                                                                                                                              /sex="male"
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Sciurognathi; Muridae; Murinae; Mus
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AUTHORS
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18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF825905 292 bp. mkNA EST 13-JAN-2001
CM4-HN0020-181100-444-d04 HN0020 Homo sapiens cDNA, mRNA sequence.
BF825905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dias Neto,E., Garcia Correa,R., Verjovski-Almerua, J., Jacober, R., Verjovski-Almerua, J., Jacober, R., Ragai,M.A., da Silva,W.J., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.,F., Matsukuma,A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotumn sequencing of the human transcriptome with ORF sequence tags % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwiq.org.br/scripts/gethtml2.pl?tl-CM4&t2-CM4-HN0020-181100-444-d04&t3-2000-11-18&t4-1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                   High quality sequence start: 3
High quality sequence stop: 292.
Location/Qualifiers
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as Neto,E., Garcia Correa,R., Verjovski-Almeida,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
/note="Organ: head_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                       /organism-"Homo sapiens"
/db_xrei-"taxon:9606"
                                                                                                                                                                                                /clone_lib="HN0020"
                                                                                                                                                                      /dev_stage="Adult"
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Pred. No. 1.
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RESULT 1
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Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.

Kiyosawa, H., Kojima, Y., Kondo, S., Salo, K., Oda, H., Okazaki, Y.,

Ono, T., Owa, C., Saito, H., Sakai, C., Salo, K., Shibata, K., Shibata, K., Shigemboo, Y., Shibada, K., Shigadawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,

Y., Shigemboo, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,

Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse EST'S (Konno, H., et al.)

Unpublished (2000)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Shehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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BB116563 RIKEN full-length enriched, adult male urinary bladder Mus
musculus cDNA clone 9530056H01 3' similar to M28383 Mouse AE3 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                  UKI:http://genome.gsc.riken.go.jp/
Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru, Carninci,P., Shibata,Y., O:awa,Y., Muramatsu,M., Okazaki,Y., and Hayashizaki,Y., Shibata,Y., O:awa,Y., Muramatsu,M., Okazaki,Y., and Hayashizaki,Y.
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                                                                                                                                                                                                                                                          Automated filtration-based high-thro.ghput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 81-45-503-9216
Email: qenome-res@gsc.riken.go.jp,
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Tel: 81-45-503-9222
                                                                                                                                                                        further details.
                                                                                                                                                                                                                                       19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                         Y. and Hayashizaki,Y.
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a 64 c 87 g 41 t
                                                  /organism="Mus musculus"
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                         /clone="9530056H01"
                                                                                                                                           Location/Qualifiers
/clone_lib="RIKEN full-length enriched, adult male urinary
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Pred. No. 1.7e+03;
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                                                       Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized prefrontal cortex library cDNA Library Preparation:

M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 791-806 (1996)
97044477
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                                                                                                                                                                                                                                                                                                     Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                               National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Chin, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enkaryota: Metazon; Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Entheria, Rod n. . Schurognathi; Muridae; Murinae; Mus
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                                        Seq primer: M13 Forward
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/lab_host-"DH10B"
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Location/Qualifiers
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DB seq length: 2000000000
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This polynucleotide comprises cDNA tragment E51 that was isolated from a human trisomy 21 foetal brain (14-wk gestation) cDNA from a human trisomy 21 foetal brain (14-wk gestation) cDNA from the comprise to bacterial and plantificial chromosomes between E7S2 and MX1. E51 was used as a probe to screen the trisomy 21 foetal brain-tibrary. 62 Clones were isolated from the 2 million clones of the original library. Overlapping clones were obtained that were used to deduce a full-length sequence (see AAV31981) coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are used to develop products for the detection, diagnosis and therapy of developmental and neurological abnormalities.
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holoprosencephaly; corpus callosum agenesis;
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This cDNA clone codes for Down syndrome-cell adhesion molecule DS-CAMI (see AAM42086), a cell surface dycoprotein belonging to a novel subclass of the 1g superfamily with highest homology to neural cell adhesion molecules. A modified direct cDNA selection technique was applied to bacterial and PI artificial chromosomes between ETS2 and MXI by using cDNA from trisomy 21 human foetal brain. A unique cDNA [ragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 G; 91 T; 0 other;
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Hest Local S
Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (regenerating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and therapy of developmental and neurological abnormalities such as Down syndrome, mental retardation, holoprosencephaly, agencsis of the corpus callosum, or schizencephaly. Antisense oligonucleotides are used for inhibiting translation of mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6604 BP; 1673 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ps-CAM2; Down syndrome-cell adhesion molecule; neural cell;
signal transduction; trisomy 21; mental retardation;
holoprosencephaly; corpus callosum agenesis;
schizencephaly; diagnosis; assay; human; ds; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Down syndrome-cell adhesion molecule DS-CAM2 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV31988 standard; cDNA; 6413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1998 (first entry)
                                                                                            New isolated Down's Syndrome-cell adhesion molecule - used develop products for detection, diagnosis and therapy of developmental and neurological abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1996;
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                                              Claim 3; Page 83-90; 109pp; English
                                                                                                                                                                                                     WPI; 1998-271791/24.
P-PSDH; AAW42087.
                                                                                                                                                                                                                                                                                                                            (CEDA-) CEDARS SINAI MEDICAL CENT
This cDNA clone codes
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                                                                                                                                                                                                                                                                                                                                                                                  96US-0029322
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453..5168
/*tag* a
     tor bown syndrome-cell adhesion molecule
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CC trapping, and the complete DS-CAM2 cDNA sequence was identified. CC trapping, and the complete DS-CAM2 cDNA sequence was identified. CC DS-CAM2 is a splice variant of membrane-bound NS-CAM1 (see ANM42086) CC DS-CAM2 is a splice variant of membrane-bound NS-CAM1 (see ANM42086) CC and is delected for the entire transmembrane domain. The DS-CAM CC and is delected for the entire transmembrane domain. The DS-CAM CC defects of the invention also provides murine DS-CAM partial CC transgenic animals, antisense oligonucleotides, and primers useful CC transgenic animals, antisense oligonucleotides, and primers useful CC transgenic animals, antisense oligonucleotides, and primers useful CC associated with developmental and neurological processes. They can CC be used in e.g., neurial prosthetic devices used in entubulation CC be used in e.g., includes can also be used in detection, diagnosis and CC nerves. The products can also be used in detection, diagnosis and CC therapy of developmental and neurological abnormalities such as CC the corpus callosum, or schizencephaly, agenesis of CC the corpus callosum, or schizencephaly. Antisense oligonucleotides or eused for inhibiting translation of mRNA.
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Best Local Similarity
Thehes 19; Conserva
Dр
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brain. A unique cDNA fraquent, designated E51 (see AAV31982), obtained and used to screen a trisomy 21 human foetal brain (1 gestation) cDNA library. Further clones were obtained by exon
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                                                                                                                                                                                                                                                                                                                                                                                                                DS-CAM; town syndrome cell adhesion molecule; neural signal Lianschedion; trisomy 21; mental retardation; holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; mouse; ds; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse bown syndrome cell adhesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV31987 standard; CDNA; 2173 HP
                                New isolated hown's Syndrome-cell adhesion molecule - used to develop products for detection, diagnosis and therapy of developmental and neurological abnormalities
                                                                                                                                                                                                                                                                                                                                           WO9817795-AI
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                                                                                                                                                                                                                                                                   23-OC1-1997;
                                                                                                                                                                                                                                                                                                       30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                              Mus sp
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                                                                                                                WPI; 1998-271791/24.
                                                                                                                                                  Korenberg Jk;
                                                                                                                                                                                         (CEDA-) CEDARS SINAI MEDICAL CENT
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                                                                                                                                                                                                                                 9608-0029322
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95.0%;
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Pred. No. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in lecule DS-CAM 3' cDNA.
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Claim 2; Page 81-83; 109pp; English.

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Best Local
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the corpus callosum, or schizencephaly. Antisense oligonucleotides
are used for inhibiting translation of mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; CSGP-1; cell surface glycoprotein; CSGP-2; antianemic; nootropic; neuroprotective; anticonvulsant; gene therapy; treatment; diagnosis; hematologic disorder; anemia; myeloproliferative disorder; lymphoma; karyotypic disorder; Klinetelter syndrome: Turner syndrome; peuronal disorder; akathesia; Alzheimer's disease; amuesia; catatonia
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    Polynucleotide encoding
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nes 18; Conservative
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58 ctylatyacctycaagaag 676
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/product= "CSGP-2"
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94.7%;
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             cell surface glycoproteins
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Pred. No. 83;
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                                                                                                                                                                                                                  Corley NC,
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                                                                                                                                                                                                                           Guegler
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                     is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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This invention describes the novel human cell surface glycoproteins (SSGP-1 and CSGP-2. The products of the invention have antianemic, nootropic, neuroprotective and anticonvulsant activity and can be used for gene therapy. The encoding nucleic acids are useful for the diagnosis, treatment and prevention of hematologic disorders such as anemia, myeloproliferative disorders and lymphoma, karyotypic disorders such as Klinefelter syndrome and Turner syndrome, and neuronal such as klinefelter syndrome and Turner syndrome, and neuronal disorders such as akathesia, Alzheimer's disease, amnesia, catatonia, epilepsy and neurofibrumaiosis. The products of the invention are also useful as probes for mapping the gene sequences encoding CSGP-1 and the meabor of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis, treatment and prevention of hematologic karyotypic disorders and neuronal disorders -
                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                  method of the invention.
                                                                                                                                                                                                                                                                                                                                                                         5; Fig 3A-D;
                                                                                                                                                                                                                                                                                                                                                                            38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders
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Query Match
Best Local Similarity
Matches 18; Conserv
863 cctyaatyacctycayraay 882
       1 cctgtatuacctucaggaag
                                    Conservative
                                              84.0%;
90.0%;
                   20
                                  0;
                                             Prod. No. 1.5e+02;
                                      Mismatches
                                       2:
                                                       Length
                                        0;
                                        Gaps
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В QΥ

the

Sequence 1438 BP;

355 A;

369 C;

385 G;

329 T; 0 other;

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AAA96337
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                                                                                                                                                                         Secreted protein; transmembrane protein; pro1484; pro4334; pro1890; pro1890; pro1887; pro4357; pro4405; pro4352; pro4357; pro4405; pro4352; pro4380; pro4340; pro4408; pro5737; pro4425; pro5990; pro4424; pro4400; pro4409; tumour; obesity; diabetes; insulinemia; kidney disorder; Recorer disease; nephropathy; companies; kidney disorder; Recorer disease; nephropathy; kidney disorder; Recorer disease; kidney disorder; Recorer disease; kidney disorder; 
                                                                                    Schonlein-Menoch purpura; cediae disease; dermatitis herpetiformis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding a novel | Typeptide designated PRO4334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-2001
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Crohus disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO1122;
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PRO6030;
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23-MAR-1999;
23-MAR-1999;
24-MAR-1999;
31-MAR-1999;
31-APR-1999;
27-APR-1999;
27-APR-1999;
27-APR-1999;
27-APR-1999;
04-MAY-1999;
04-MAY-1999;
                                                                                                      sig_peptide
                                                                                                                       Key
                                                                                                                                  Homo sapiens
                                                                  01-MAR-2000;
                                                                                       WO200056889-A2
                                                                            28-SEP-2000
                                                                  2000WO-US05601
     9908-0125774
9908-0125778
9908-0125782
9908-0127035
9908-0127703
9908-0130359
9908-0131270
9908-0131270
9908-0131271
9908-01312371
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/*Lag.
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84..1406
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Query Match
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25 - MAY - 1999;
08 - JUN - 1999;
20 - JUL - 1999;
03 - AUG - 1999;
09 - DEC - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for diagnosing tumour in a mammal. The polypeptides, their agonists and antaqonists are useful treating a condition associated with expression or activity of the polypeptide. Conditions treated include obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are capable of inducing proliferation of mammalian kidney mesangial cells and are therefore useful for treating kidney disorders associated with decreased mesangial cell function such as Bergers disease or other nephropathies associated with Schonlein-Henoch purpura, cellac disease, dermatitis herpetiformis or Crohns disease. The nucleic acids may be used to generate transgenic animals for use in development and screening of therapeutically useful reagents and also for chromosome identification and disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel secreted and transmembrane polypeptides useful for diagnosing tumour in a mammal, for identifying agonists and antagonists of the polypeptide and for therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a secreted or transmembrane polypeptide. The specification describes polypeptides designated PRO1484, PRO4334, PRO122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405, PRO4356, PRO4352, PRO4390, PRO4334, PRO4408, PRO5737, PRO4425, PRO5990, PRO60300, PRO4424, PRO4422, PRO4430 and PRO4499, PRO1889 polypeptide is
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
  04-FEB-2000;
                           30-JAN-2001; 2001WO-US00670
                                                     09-AUG-2001
                                                                                WO200157278-A2
                                                                                                                                   cervical cancer;
                                                                                                                                               Probe;
                                                                                                                                                                        Probe
                                                                                                                                                                                                 12-OCT-2001
                                                                                                                                                                                                                          AAI13890;
                                                                                                                                                                                                                                                    AAI13890 standard;
                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                     863
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DB; AAB1891U.
                                                                                                                                                                                                                                                                                                                 cctgaatgacctgcagcaag 882
                                                                                                                                                                                                                                                                                                                                cctgtatgacctgcaggaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Fig 3; 222pp; English.
                                                                                                                                             human; microarray; gene expression; cervical epithelial cell;
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99US-0135750.
99US-0138166.
99US-0144791.
99US-0146970.
99US-0170262.
                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                       393 A; 406
                                                                                                                                                                                                                                                      DNA;
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                                                                                                                                                                        expression analysis in 'uman cervical cell: imple
                                                                                                                                                                                                                                                       1954 BP
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Wood WI,
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Pred. No. 1.5e+02;
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Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                          376
                                                                                                                                                                                                                                                                                                                                                                                                                                          T; 0
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Best Local :
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from human HeLa cells. The SENPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SENP). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1954 BP; 634 A;
                                                                                                                                                                                                       genetic
                                                                                                                                                                                                                                      Probe #3938 used to measure gene expression in human placenta
                                                                                                                                                                                                                                                                              AA135252;
                                                                                                                                                                                                                                                                                                  AAI35252 standard; DNA; 1954
                  (MOLE-)
                                       04-OCT
                                                 21-SEP-2000;
27-SEP-2000;
                                                                                                                       30-JAN-2001;
                                                                                                                                            09-AUG-2001
                                                                                                                                                                WO200157272-A2
                                                                                                                                                                                     Homo
                                                                                                                                                                                                                   Probe;
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hes 18; Conserv
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|00 ccagtatgacctycagaaag
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                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful t
zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                 microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS INC
                                                                                                                                                                                                        disorder;
                   MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID No 3823; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                      2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                         (11:51
                                                                                                                         2001WO-US00663
                                                                                                    2000US-0180312
                                                                                                                                                                                                         ss.
                   DYNAMICS
                                                                                                                                                                                                                   human;
                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                      84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                               350 C;
                                                                                                                                                                                                                                                                                                                                                      219
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Pred. No. 1.5e
O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                447 G;
                                                                                                                                                                                                                    antenatal
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                                                                                                                                                                                                                    diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                other;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1954;
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Penn SG,

Hanzel DK,

Chen W,

Rank DR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1954 BP; 634 A; 350 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prohybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, munitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases
                                                                                                                                                                                                                                                                                                                                                                                                                        Probe #3744 used to measure gene expression in human breast sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI03753 standard; DNA; 1954
                                                                                                                                                                                                               04
                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           Probe; human; inflammatory
                                                                                                                                              :IdM
                                                                                                                                                                   Penn
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                                                                                          Claim
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                                                                                                                         Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic acid zing gene expression in human placenta -
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                                                                                                              single exon nucleic human breast .
                                                                                                                                              2001-476286/51
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                                                                                                                                                                                          MOLECULAR DYNAMICS
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                                                                                          SEQ ID NO
                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                              2000US-0180312
2000US-0207475
2000US-0608408
2000US-0632366
2000US-0234587
2000US-0236559
2000US-0236559
2000US-0236559
                                                                                                                                                                                                                                                                                                                                                                                           ; breast of disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                     2001WO-US00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3938; 654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%;
90.0%;
                                                                                            3744;
                                                                                                                                                                                                                                                                                                                                                                                                       disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                            proliferative breast disease;
                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219
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                                                                                                                            acid
                                                                                            322pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
0; Mis
                                                                                                                                                                                             INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 G;
                                                                                                                                                                       Rank
                                                                                                                            probe used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.8;
No. 1
                                                                                                                                                                        CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   523 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db
1.5e+C2;
2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes useful
                                                                                                                             measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                non-carcinoma
                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                               expression
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                                                                                                                                                                                                                                                                                                                                                                                                           SS;
                                                    probe
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RESULT
AAI1498
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Best Local
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specification, but was obtained in electronic format directly
at ftp.wipo.int/pub/published not seamonant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             include: breast cancer, disorders of development, inflammatory di
of the breast, fibrocystic changes, proliferative breast disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI14982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001
                                                                          The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene sample derived from human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                            30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #4915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI14982
                    expression, the probes are therefore useful in grading and/or of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of t specification, but was obtained in electronic format directly at ftp.wino.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                               Penn
                                                                                                                                                                                                                                                                                                 21-SEP-2000;
                                                                                                                                                 Claim
                                                                                                                                                                       analyzing
                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                 5.
                                                                                                                                                                                                         2001-488901/53
                                                                                                                                                                      denome-derived single exon nucleic acid probes useful for
zing dene expression in homan cervical epithelial cells .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                 SEQ 1D No 4915;
                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tor
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20000IS - 0236359 .
20000IB - 0024263 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8P;
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                               2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression
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Pred. No. 1.5e
0; Mismatches
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                                                                                                                                                                                                                                  Rank DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analysis in human cervical cell sample.
                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.8;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5e+02;
2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Η.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                       part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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BP;

714 A;

366 C;

526 G;

349 T;

0 other

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                          RESULT 13
AA104749
ID AA1047
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AAI36328
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                                                                                                              Query Match
Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1641 ccagtatgacctgcagaaag 1660
                                                                        The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #5014 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI36328 standard; DNA; 1955
                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA136328;
         AA104749;
                                                                                                                                                                                                                                                            analyzing
                                                                                                                                                                                                                                                                                                                                                 04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                            AAI04749 standard;
                                                                                                                                                              Sequence
                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                              (MOLE-)
                                                                                                               Local Similarity 90.0 nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 cctgtatgacctgcaggaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                            SC,
                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                           genome-derived single exon nucleic acid zing gene expression in human placenta .
                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder;
                                                                                                                                                               1955
                                                                                                                                                                                                                                         SEQ ID No 5014; 654pp; English
                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312
                                                                                                                                                               вР;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS
                                                                                                                                                               714 A;
                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%;
90.0%;
                                                                                                                         84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                            Chen W,
                             1955
                                                                                                                                                               366 C;
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                                                                            1660
                                                                                             20
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                                                                                                                0;
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Pred. No. 1.5e+02;
0; Mismatches 2;
                                                                                                                98
                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                526 G;
                                                                                                                                                                 349 T;
                                                                                                                                                                 0 other;
                                                                                                                                                                                                                                                                       probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1955;
                                                                                                                  Indels
                                                                                                                                   Length 1955;
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                                                                                                                  Gaps
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RESULT 14 AAH57390

AAH57390 standard; cDNA; 6016

Вŀ

DЬ

1641 ccaqtatgacctgcagaaag 1660

10-SEP-2001

(first entry)

skeletal

muscle cell specific cDNA sequence

SEQ

ID NO:230.

Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory;

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                                        Matches
                                                     Query Match
Best Local Similarity
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26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                       The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, staging, those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe; human; breast disease; breast cancer; development disorder;
inflammatory disease; proliferative breast disease; non-carcinoma
                                                                                                                                                                                                                                                                                                                                                                     Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-2001 (first entry)
                                                                                                                                               Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                          Sequence 1955 BP; 714 A;
                                                                                                                                 at ftp.wipo.int/pub/published_pet_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                        ına
1 cctutatgacctgcaqqaaq
                                                                                                                                                                                                                                                                                                                                                        human breast
                                                                                                                                                                                                                                                                                                                                                                                                                          SG,
                                                                                                                                                                                                                                                                                                                                                                                                2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                           single exon nucleic
human breast –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #4740 used to measure gene expression
                                                                                                                                                                                                                                                                                                                            25;
                                        18;
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                                                                                                                                                                                                                                                                                                                            SEQ 1D No 4740;
                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                      Conservative
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0207456
                                                     84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                           366 C; 526 G;
                                                                                                                                                                                                                                                                                                                                                                   acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                           322pp; English.
            20
                                        0;
                                                     Score 16.8; DB 22
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                           Kank DK;
                                         Mismatches
                                                                                                             349 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in human breast sample
                                                                   22;
                                           2;
                                           Indels
                                                                   Length
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                                                                                                                                                   part of the printed directly from WIPO
                                                                       1955;
                                           0;
                                           Gaps
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RESULT 1
AAZ 24616
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences (1). (1) can have cytostatic, immunomodulatory and sequences (1). (1) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (1) and proteins (11) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, minetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (1) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (1) and (11) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, and continue the gene profile and continues the gene is associated with a continue of the can be used for diagnosis.
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3100 ectygatyaeetycagycag 3119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-291057/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200132927-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with a cancer, immunopathology or neuropathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sornasse T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6016 BP; 1953 A; 1297 C; 1590 G; 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer, immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predisposition to a disorder where the gene is associated with a
               17-MAR-1999;
                                               23-SEP-1999
                                                                              W09947674-A2
                                                                                                                                          Human; lung tumor;
                                                                                                                                                                          Human lung tumor associated polynucleutide
                                                                                                                                                                                                           07-DEC-1999
                                                                                                                                                                                                                                           AAZ24616;
                                                                                                                                                                                                                                                                         AAZ24616 standard; cDNA; 8948 BP
                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 158-159; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seithamer JJ,
                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0163508
             99WO-US05798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                            lung cancer; T cell stimulation;
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90.0%;
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Pred. No. 1.6e+02;
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18-MAR-1998;
27-JUL-1998;
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                                                                                                                                                  The invention provides isolated human lung tumor nucleic acids and polypeptides. The polypeptides can be used for the treatment of lung cancer. The polypeptides and polypucteotides can be used to stimulate T cells or antigen presenting cells for use in the treatment of lung cancer. The polypeptides and monoclonal antibodies specific for the polypeptides can also be used to inhibit the development of lung cancer. Agents which bind the polypeptides can be used for detecting lung cancer and for monitoring the progression of lung cancer.
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Claim 12; Page 111-114; 148pp; English.
                                                                                                                                                                                                                                                                                                                    New isolated lung tumor polynucleatides, used to develop
the treatment, prevention and monitoring the progression
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                                                                                                                            Sequence 8948 BP; 2786 A;
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Search completed: March Job time: 17515 sec 4 2002, 05:21:26

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SS:	H4.0%; imilarity 90.0%; ; Conservative 0 Latgacetycaygaad 20 [[[[]]]]]]]]]	n US/0918 il C. il C. ina A. riah R. riah R. SURFA 31 US GUMBER: US 1 1998-11-0 6 6 m		24-	- 23 -	4446	1186 3 U 1186 3 U 1415 1 U 1515 4 U 1521 3 U 1521 3 U
US/08998416  Peter Aliner bline tline trine refer brine corinne Corinne CNOMIC DNA SEQUENCES THEREOF	Score 16.8; Pred. No. 17 0; Mismatche	7331 CE GLYCOPROTE /09/187,331	ALIGNMENT	09-442	08-404 09-263 08-864 08-404	)9-503 )9-080 )8-404 )8-422 )9-032	US-08-475-975 US-09-084-889 US-08-257-341 US-09-080-629 US-09-646-538 US-08-646-538 US-09-503-222
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A GOSSADI	Length 1438; Indels 0;			Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence Sequence Sequence
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STREET: 3054 Cornwallis Road C17Y: Research Triangle Park STATE: No. 6239264th Carolina

ADDRESSEE:

No. 6239264artis Corporation

COUNTRY:

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Best Local Similarity 89.5%;
Matches 17; Conservative
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REFERENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEC. TO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 530:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: CH 00
FILING DATE: 31-DEC-1996
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                 APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Enhanced Starch Biosynthesis
NUMBER OF SEQUENCES: 51
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: UBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ORIGINAL SOURCE:
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                                                               CURRENT APPLICATION DATA
PRIOR APPLICATION DATA:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meigs, J. Time
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLUGY:
                                                                                                                                                                                                                        CITY: St. Louis
                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                      STREET:
                  CLASSIFICATION:
                                APPLICATION NUMBER: US
FILING DATE: 19930712
                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                          1, Application US/08090523
5. 5498830
                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                     63198
                                                                                                                                                                                                  Missouri
                                                                                                                                                                                                                                    E: Grace L. Bonner, Monsanto Co. BB4F
700 Chesterfield Parkway No. 5498830th
                                                                                                                                                                                     USA
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SYSTEM: PC-DOS/MS-DOS
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                                                US/08/090,523
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Pred. No. 47;
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US-08-090-523-1
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
TELEPHONE: (314) 537-604286
TELEPHONE: (314) 537-604281
TELEPHONE: (314) 537-604281
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US 07/539
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
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                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DUS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kishore, Ganesh M.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Enhanced Starch Biosynthesis
NUMBER OF SEQUENCES: 51
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                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ALBRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bonner, Grace L. REGISTRATION NUMBER: 32,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 07-JUI
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/090,523 FILING DATE: 19930712
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Pred. No. 49
                                             38-21(10559)A
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Best Local Similarity
Matches 17; Conservat
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                                                                                                                                                          NAME: BORNEY, Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38-21(10559)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
TELEPHONE: (314) 537-6047
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539763
FILING DATE: 18-JUN-1990
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                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 08/090,524
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kishore, Ganesh M. APPLICANT: Stark, David M. TITLE OF INVENTION: Enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                   FEATURE:
                                                  MOLECULE TYPE:
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STATE: Mis
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TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 1..1293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 03-MAR
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STREET: 700 Chesterfield Parkway No. 5608149th
NAME/KEY: CDS
LOCATION: 1..1293
                                                                     TOPOLOGY:
                                                                                      STRANDEDNESS:
                                                                                                                        LENGTH:
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Pred. No. 49;
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RESULT 6
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US-08-398-627-3
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Best Local Similarity
Matches 17; Conserv
                                                         Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                             TELEFAX: (314) 537-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kishore, Gamesh M.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Enhanced Starch Biosynthesis
NUMBER OF SEQUENCES: 51
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APPLICATION NUMBER: US 08/090,523
APPLICATION NUMBER: US 07/709663
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/398,627
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FEATURE:
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                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
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CTTY: St. Louis
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COMPUTER: 1HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
667 CTGTATGAACTGCTGGAAG 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                    TOPOLOGY:
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              2 ctgtatqacctgcagqaaq 20
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700 Chesterfield Parkway No. 5608149th
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N: 800
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Pred. No. 49;
                                                                                         Score 15.8;
                                                                              Pred. No. 49;
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                                                                                            DB 1;
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US-08-406-858-1
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                                                                                                      US-08-406-858-3
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                                                   Sequence 3, Application Patent No. 5648249
GENERAL INFORMATION:
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: Zalewski, James C.
TITLE OF INVENTION: Method of Improving the Quality of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 1HM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 APPLICANT:
APPLICANT:
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ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5648249th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
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APPLICATION NUMBER: US 08/070,155
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PCT/US94/05275
FILING DATE: 18 MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                           667 CTGTATGAACTGCTGGAAG 685
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STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bonner, Grace L. REGISTRATION NUMBER: 32,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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                                                                                    Application US/08406858
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                                                                                                                                                                                                                                               Conservative
Barry, Gerard F.
Kishore, Ganesh M.
Stark, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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89.5%; Pred. No. 49;
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PCT-US91-04036-1
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Best Local Similarity
Matches 17; Conserv
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COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-1005/MS-100S
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BONNEY, GTAGE L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
TELEFAX: (314)537-6047
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APPLICATION NUMBER: US 0
FILING DATE: 28-MAY-1993
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                         APPLICANT: Kishore, TITLE OF INVENTION:
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                                                                                 COUNTRY:
                                                                                                                      ADDRESSEE: Monsanto to.
STREET: 700 Chesterfield Village Parkway
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700 Chesterfield Parkway No. 5648249th
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89.5%;
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Increased Starch Content in Plants
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Best Local S
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GENERAL INFORMATION:
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                                                                                                                         TELEFAX: (314) 537-6047 INFORMATION FOR SEQ ID NO: 3:
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TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pater. In Release #1.0,
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7357
TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUMBER OF SEQUENCES:
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NAME: McBride, Thomas P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                         MOLECULE TYPE:
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LOCATION:
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Local Similarity 89.5%;
hes 17; Conservative
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NAME/KEY: CDS
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                             DNA (genomic)
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Pred. No. 49;
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PCT-US94-05275-3
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Best Local Similarity
Matches 17; Conserv
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GENERAL INFORMATION:
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Best Local Similarity
Matches 17; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
APPLICATION NUMBER: US 0
FILING DATE: 28-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                           CURRENT APPLICATION DATA:
                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                         667 CTGTATGAACTGCTGGAAG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: JBM PC compatible
OPEFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rel-dase #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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               CLASSIFICATION:
                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       ENGTH:
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89.5%;
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                                                                                                                                                                    Potatoes
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                                                                                                                                                                                 Method of Improving the Quality of Stored
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Query Match
Best Local Similarity
Matches 17; Conserve
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US-07-735-065-3
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US-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US FILING DATE: 28-MAY-19 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                   TELEFAX: (916) 753-1510 (NEORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                          FILING DATE: DATA:

PRIOR APPLICATION NUMBER: unassigned
APPLICATION NUMBER: 1991

THE DATE: 16-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Glycogen Biosynthetic Enzymes TITLE OF INVENTION: In Plants
NUMBER OF SEQUENCES: 5
                                                                                                                                               REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/632,383
FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Christine K. Shewmaker APPLICANT: David M. Stalker
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TOPOLOGY: 1:
MOLECULE TYPE:
-735-065-3
                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
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                                       STRANDEDNESS:
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                                                      NUCLEIC ACID
                                                                                                                                                                                          Donna E. Scherer
                                                                                                                                                                                                                         Elizabeth Lassen
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1920 Fifth Street
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         genomic DNA
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Pred. No. 49;
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US-08-469-202-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 17; Conserv
                                                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                               MOLECULE TYPE: DN
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/016,881
FILING DATE: 11_FEB_1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: STALKER, DAVID
TITLE OF INVENTION: GLYCLGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 916-753-6313
                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
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682 CTGTATGAACTGCTGGAAG 700
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                                                                                                                                                                             LENGTH: 1323 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
                                                                                                                                                                                                                                                                      TELEPHONE: 916-753-1510
                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 3
NAME: Donna E. Scherer
REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1920
CITY: DAVIS
                                                                                                                                                                                                                                                                                                                                 NAME: Carl J. Schwedler REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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89.5%;
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89.5%; Pred. No. 49;
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Pred. No. 49;
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RESULT 15 US-08-484-434C-13 ; Sequence 13, Application US/08484434C

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COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIM PC
OPERATING SYSTEM: Windows NT 4.0; MS Word for Windows 7.0a
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/484,434C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION UNMBER: 08/016,881
FILING DATE: 11-FEB-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Schwedler, Carl J.
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 35,924
REFERENCE/DOCKET NUMBER: 31,924
REFERENCE/DOCKET NUMBER: 31,924
REFERENCE/DOCKET NUMBER: 31,924
REFERENCE/DOCKET NUMBER: 31,933/01
TELECHONE: 530-792-2463
INFORMATION REFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1323 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: CIrcular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: 16..1308
US-08-484-434C-13
Search completed: March 4, 2002, 05:11:34 Job time: 16948 sec
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GENERAL INFORMATION:
APPLICANT: STALKER, DAVID
TITLE OF INVENTION: GLYCOGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: Calgene LLC
STREET: 1920 Fifth Street
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Best Local Similarity 89.5%; Pred. No. 49
tches 17; Conservative 0; Mismatche
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CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
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Title:
Perfect score:
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## ALIGNMENTS

RESULT AAV31985 ID AAV3

AAV31985 standard; cDNA; 842

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DS-CAM; hown syndrome-cell adhesion molecule; neural signal transduction; trisomy 21; mental retardation; holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; mouse; ds; ss.
                                                                                                                                                                                                                                                                       Mouse Down syndrome-cell adhesion molecule DS-CAM 5'
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New isolated hown's Syndrome-cell adhesion molecule - used to develop products for detection, diagnosis and therapy of developmental and neurological abnormalities
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This cDNA sequence comprises the 5' region of a cDNA clone commutine Down syndrome-cell adhesion molecule (DS-CAM), a comember of a novel subclass of the Ig superfamily with homology to come commutate cell adhesion molecules. The middle region (see AAV31986) cc and 3' region (see AAV31987) of the clone are also provided. The commutate DS-CAM clone was isolated from a C57 Black/6 mouse brain cc cDNA library using human DS-CAM commutate of the clone are also provided. The cc cAM42086-87), as well as expression vectors and host cells, cc transgenic animals, antisense oligonucleotides, and primers useful cc associated with developmental and neurological processes. They can cc methods of repairing (regenerating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and cc therapy of developmental and neurological abnormalities such as communication, mental retardation, holoprosencephaly, agenesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides are used for inhibiting translation of mRNA.
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DS-CAM2 (see AAW42087), an extracellular, soluble protein belonging to a novel subclass of the 1g superfamily with highest homology to neural cell adhesion molecules. A modified direct cDNA selection technique was applied to bacterial and Pl artificial chromosomes between ETS2 and MX1 by using cDNA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk gestation) cDNA library. Further clones were obtained by exon trapping, and the complete DS-CAM2 CDNA sequence was identified. DS-CAM2 is a splice variant of membrane-bound DS-CAM1 (see AAW42086) and is deleted for the entire transmembrane domain. The DS-CAM gene spans 900-1200 kb of genomic DNA and maps at chromosome
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                                                                                                      gestation) cDNA library. Further clones were obtained by exon trapping. The complete DS-CAM1 cDNA sequence was deduced from overlapping clones. A splice variant cDNA (see AAV11988), encoding non-membrane bound DS-CAM2 (see AAW42087), was also identified. The DS-CAM gene spans 900-1200 kb of genomic DNA and maps at chromosome 21q22.2-22.3. The invention also provides murine DS-CAM partial sequences (see AAV31985-87), expression vectors and host cells,
                                                                                                                                                                                                                                                                                                        DS-CAM1 (see AAW42086), a cell surface glycoprotein belonging to a novel subclass of the 1g superfamily with highest homology to neural cell adhesion molecules. A modified direct cDNA selection technique was applied to bacterial and Pl artificial chromosomes between ETS2 and MX1 by using cDNA from tricomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk
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                    transgenic animals, antisense oligonucleotides, and primers useful for amplification of DS-CAM nucleic acid. DS-CAM polypeptides are associated with developmental and neurological processes. They can
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develop products for detection, diagnosis and therapy
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Matches

Conservative

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Score 307.6; DB 1 Pred. No. 5.6e-79; 0; Mismatches 264

DB 19; 264;

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Gaps

Query Match Best Local Similarity

36.5%; 65.1%;

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AC CONP
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                                                                                                                                                                      This is cDNA clone ethbu0018f2. It was isolated from human foetal brain cDNA using a novel merbod for identifying genes encoding novel secreted or membrane associated proteins. The method involves: (i) liquiting a library of cDNA to DNA such as vector purAP3 (see ANV27206) encoding a kaline phosphatase (AP) that lacks signal peptide and membrane anchor sequences (see AAW55047); (ii) transforming bacteria with the products; (iii) transfering, separately, DNA from (some of) the bacterial clones into mammalian cell library that expresses AP; and (v) identifying the corresponding clone in the bacterial library, isolating the corresponding clone in the bacterial library, isolating the corresponding clone in the bacterial library, isolating the
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                                                          as a partial CDNA clone of a novel neural adhesion molecule (see AAW55045) that contains multiple, consecutive IgG domains. The novel method is very sensitive and is suitable for high throughput screening techniques and automation.
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                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as a localised neuropathies and central nervous system diseases, such as a localised neuropathies and central nervous system diseases, such as a localised neuropathies and central nervous system diseases, such as alternal sclerosis, and Shy-Prayer Syndrome. Other uses include the utilisation of the activity brayer Syndrome. Other uses include the lateral sclerosis, activities such as: Inmune system suppression, activity, chemolactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C N S discretars
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19-OCT-2000;
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central nervous
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Zhou P,
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                                                 standard;
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2000US-0552317.

2000US-0598042.

2000US-0620312.

2000US-0652450.

2000US-0652191.

2000US-0693036.

2000US-0727344.
                                                                                                                                                                                                                                                                                                           Conservative
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Wehrman T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Conserv
    simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW80810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              æ
                                                                                                                   cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roizman
                                                                                                                                                              (first entry)
                                                    protein number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of the Herpes simplex virus
                                                                                                                 protein number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0843659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US07573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 361..4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "HSV ICP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.78;
                                                                                                                                                                                                                                                     cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSV infection; ss.
                                                                                                                                                                                                                                                        4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                         4; ICP4; alpha-4;
                                                                                                                      4 alpha-4 gene
                                                                                                                                                                                                                                                        ВΡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.2;
No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                         2130
                                                                              cell apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2170
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QΥ
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    RESULT 8
AAZ29335/c
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                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                The herpes simplex virus (HSV) alpha-4 gene encodes infected cell protein number 4 (1CP4). Both the alpha-4 gene and ICP4 can be used to block cell apoptosis. Similarly the administration of an agent that inhibits ICP4 or the alpha-4 gene can induce apoptosis in HSV infected cells. This can be used for the immortalisation of cells, production of proteins, gene therapy, or inhibition of cell death induced in vivo. They can also be used for production of therapeutics comprising inhibitors of HSV ICP4 function, useful for treating HSV function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09804709-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of herpes simplex virus ICP4 polypeptide - useful for blocking apoptosis in cells, production of proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-1998
                                                                                                                                                                                                                                                                      2169
                                                                                                                                                                                                                                                                                                                 2229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leopardi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ARCH-) ARCH DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4257 BP; 412 A; 1768 C; 1663 G; 414 T; 0 other;
                                                                                                                                                                                                                 AAZ29335
                                                                                                  Acrosome reaction protein; P3; sperm protein; polycystin-1; suREJ; Polycystic Kidney Disease and Receptor for Egg Jelly protein; PKDR zona pellucida; fertility; contraceptive; gene therapy; ds.
                                                                                                                                             Human acrosome reaction protein-PKDREJ encoding DNA
                                                                                                                                                                      29-FEB-2000
             polyA_signal
                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                     4.7%;
Local Similarity 62.0%;
hes 62; Conservation
                                                                                                                                                                                                                                                                                          62
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                                                                                                                                                                                                                                                                     1998-130697/12.
                                                                                sapiens
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                                                                                                                                                                                                                 standard; DNA;
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                                                                                                                                                                     (first entry)
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/*rag- a
/product- '
7636..7641
/*tag- b
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/product= "Infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                        Location/Qualifiers
                                                1..6762
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                                                                                                                                                                                                                 7686
                           "Acrosome
                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                           Score 39.2; DB Pred. No. 0.37; 0; Mismatches
                                                                                                                                                                                                                  뜓
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell protein"
                          reaction protein (PKDREJ)"
                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                       2130
                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for,
                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                  4257;
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                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell protein
to block
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  AAQ76213
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a DNA encoding functional human acrosome reaction protein, PKDREJ or P3, PKDREJ is a verm protein involved in binding the sperm to the egg and/or triggering the acrosome reaction. It exhibits homology to human polycystin-1 and sure. It can be used to identify antibodies or proteins that block the acrosome reaction and compounds that trigger acrosome reaction in the absence of zona pellucida. Molecules that enhance the efficacy of the acrosome reaction protein can be used to increase fertility and those blocking its action can be used as contraceptives. DNA encoding PKDREJ can be used ir gene therapy and also as primer or probe for identifying sequences that encode mutant forms of acrosome reaction protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09964457-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 3; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New functional mammalian acrosome reaction protein, useful for fertility treatment
 misc_RNA
                                                                                                                                                               HSV; junction-spanning transcript; L/ST; therapy; virucide;
                                                                                                                                                                                       HSV L/ST region
                                                                                                                                                                                                                 04-AUG-1995
                                                                                                                                                                                                                                           AAQ76213;
                                                                                                                                                                                                                                                                    AAQ76213 standard; DNA; 12001 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7686 BP; 1952 A; 1827 C; 1809 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fertility treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harris PC, Hugues JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-1999
                                     misc_RNA
                                                                         misc_binding
                                                                                                                                        Herpes
                                                                                                  TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                   453 GCCGGGTCCGAGCAGCCGCAGGCGGAAGGCCCAGGCCAGGCGCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 65; Conserv
                                                                                                                                                                                                                                                                                                                                                62 cgctggctcgctggctcgcgggaggccggggcagcaggagggcatgtg 109
                                                                                                                                                                                                                                                                                                                                                                                                 2 cgggccgggcgcggagcgcagcgcaacgcgggggggcgaggccggcgcgcgtgyctcgct 61
                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-097518/08.
                                                                                                                                       simplex virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-GB01839
                                        /*tag= b
/note= "ICP4 |
229
                                                                         /*tag= 2
220..225
/*tag= c
/note= "5' end of the L/STs"
370..372
                                                                                                  Location/Qualifiers
199..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.2; Di
Pred. No. 0.49
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ç,
                                                 binding
                                                  site
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..49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2098 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7686;
                                                                                                                                                                                                                                                                                                                                    406
                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 10
AAN70317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An HSV-specific junction-spanning transcript (L/ST) maps at the 5' end to the b repeat sequences of HSV DNA at approx. 3 and 125 kb, and extends into the c repeat sequences of HSV DNA. Compounds that inhibit HSV L/ST synthesis may be used as anti-HSV virucides. The HSV-1 DNA sequence in the region of the L/STs
                                                                                                                                                                                                                                                                                                                                                   4505 cngcygggggctygcggggccqygccncggccagccccggg 4544
                                                                                                                                                                                                                                                                                                                                                                                               4445 caggoggggcycytcggcqtucggcggcggcggggaagcgggggcccgcggggtccctccgg 4504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12001 BP; 1568 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 38-44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herpes Simplex Virus (HSV) specific junction spanning transcript for inhibiting HSV L/ST synthesis, in the treatment of HSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-022825/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09428156-A
                                                                                                                                                                  Sus scrofa domestica.
                                                                                                                                                                                                                 Sequence encoding porcine inhibin beta-chain precursor beta-A.
                                                                                                                                                                                                                                         09-APK-1991
                                                                                                                                                                                                                                                                  AAN70317;
                                                                                                                                                                                                                                                                                       AAN70317 Standard; CDNA; CBB BF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is given in AAQ76213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DAND ) DANA FARBER CANCER INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-1993;
                                                                    polyA_signal
                                                                                           mat_peptide
                                                                                                                                                                                         Fertility control; contraception;
           20-MAY-1987
                                  EP222491-A
                                                                                                                                                                                                                                                                                                                                                                                                                                           4.7%;
Local Similarity 62.0%;
hes 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                             2 egggecqqqegyryycqqaqrqcaycycaacgcgggggggcgagggcggggcggcgtggctcgct 61
                                                                                                                                                                                                                                                                                                                                                              cgctygctcgctygctcg myaggccgggcagcagcagg 101
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeh L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9305-0065146
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                                                       /*tag= b
3551..3556
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= d
/note= "first codon of ORF-1"
                                                                                          /product=hydrophobic signal 958..1307
                                                                                                                 /*tag=
                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4557 C; 4315 G; 1561 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39.2; DB Pred. No. 0.6; 0; Mismatches
                                                                                                                                                                                          hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
                                                                                                                                                                                         spermatogenesis; ss
                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 12001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                        pro-region
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0;

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HRESULT
AAQ2037
11D AAQ2
XX AAQ
AC AAQ
XX OB-
DT 08-
XX 11p
KW Cle
XX Cle
XX Pse
XX Pse
FT CDS
FT CDS
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03-OCT-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identification of prodomain regions located N-terminal to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or brodomain immunogens are useful in monitoring preproinhibin prodomain immunogens are useful in monitoring preproinhibin at modulating in transformant cell culture or in experiments directed at modulating the climical condt. or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding CDNA has led to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                          1629
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3588
                                                                                                                                                       P.glumae PG1 lipase A gene and stabilisation/translocation function
                                                                                                                                                                                                                                                                                                                                         1569
                                                                                                                                                                                 08-APR-1992
                                                                                                                                                                                                                                 AAQ20372 standard;
                                                                                               Pseudomomas
                                                                                                                     lipase-specific stabilisation/translocation protein:
cleaning system: ORF2; ss.
                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                  1987-137512/20
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                                                                                                                                                                                                                                                                                                                                      teetitetteeteeagealeggagtggggaeageagtigeteeaaegggaatattgteet 1628
                                                                                                                                                                                                                                                                                           ctcctttt 1636
                                                                                                                                                                                                                                                                                                                 ctccttgt 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 1B; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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85US-0783910.
86US-0827710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В₽;
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86EP-0307586
                                                              Location/Qualifiers 483..1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HY;
                           /*tag= a
/product= lipase_A
1559..2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     881 A; 986 C;
   /label- ORF2
                  /*tag=
                                                                                                                                                                                                                                     DNA; 2900
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                      ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         723 T;
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                                                                                                                                             detergent;
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06-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A P.glumae PGJ genomic library was constructed in cosmid vector c2RB. The lipA gene was isolated by screening with probes based on the vector library and a lipa sequence of the P.glumae lipase. Immediately downstream of the lipA yene was found a second open reading frame, designated ORF2. It is ORF2 which encodes the lipase-specific designated ORF2. It is ORF2 which encodes the lipase-specific designated ORF2. It is ORF2 which encodes the lipase-specific designated ORF2. It is ORF2 which encodes the lipase-specific designated ORF2. It is ORF2 which encodes the lipase-specific designated ORF2. It is ORF2 which encodes the lipase-specific designated ORF2. It is ORF2 which encodes the lipase-specific designated ORF2.
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translocation or stabilisation gene, u
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p-PSDB; AAR20177, A/
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                                      CHC operon; CHC gene cluster; cyclohoxanecarboxylic acid; polyketide biosynthetic intermediate; shikimate pathway; shikimic acid-CHC-COA biosynthetic pathway; doramectin production; recombinant Streptomyces avermitilis bkd mutant; AnsJ/AnsK; AnsL;
                                                                                                                 Streptomyces
                                                                                                                                             29-JAN-2001
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                          ChcA; cyclohexenylcarbonyl
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Streptomyces collinus
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                                                                                                                                                                                                        standard; DNA; 7191
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                                                                                                                 collinus CHC (cyclohexamecarboxylic acid) gene operon
                                                                                                                                               (first entry)
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90EP-0307440
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pred. No. 0.7;
0; Mismatches 100;
                                  CoA reductase; AnsM;
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gene, used to produce an efficient
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09-SEP-1999;
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P-PSDB; AAB23249, AI
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                                                                                                                                                                                                                           Corn 1-deoxy-D-xylulose 5-phosphate synthase putative coding
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                                                                                                                             Corn; 1-deoxy-D-xylulose isoprenoid biosynthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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      Location/Qualifiers
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                                                                                                                                       5-phosphate synthase; herbicide; ss.
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Pred. No. 1
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DE Human
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KW Kainat
KW assay;
XX

17-JUN-1993

(first entry)

Human KA-2 receptor gene

Kainate high affinity receptor; EAA2; excitatory amino acid family; assay; binding affinity; CNS disorders; drugs; ds.

AAQ36930

standard; DNA;

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ttgtcaalgcatcgctgcaagagtdgtgtttgcaagcacatcggggacgctggt 235 ctecgettycccgtaalctyqltlalyacgagtttgccgttcttcaccccactagctacc

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                                                                                                                                                                                                                                                                   The present sequence is a putative coding sequence for the corn 1-deoxy-D-xylulose 5-phosphate synthase enzyme (DXPS). Its protein is 1-deoxy-D-xylulose 5-phosphate synthase enzyme (DXPS). Its protein is 1 involved in the isoprenoid biosynthesis pathway. The cDNA was identified by sequencing a number of clones and then comparing their protein the sequences to known proteins; this showed the sequence's similarity to the capsicum annuum DXPS sequence. The DXPS gene and protein can be used to create transgenic plants which express the gene at either different create transgenic plants which express the gene at either different create transgenic plants which express the gene at either different transcriptions.
                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide encoding 1-deoxy-D-xylulose 5-phosphate synthase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
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Pred. No. 0.94
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of the gene encoding the human KA-2 receptor, a kainate high affinity receptor of the EAA2 (Excitatory Amino Acid) family. The sequence can be used in the identification of sequence related genes. It can also be used to produce calls able to produce the receptor, these cells and membrane fragments of them can be used to assay compounds for binding affinity to human EAA receptor i.e. to screen compounds for potential use as drugs against CNS disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotide encoding human excitatory amino acid-2 receptor - useful for determining binding affinity of cpds. for the receptor in assaying for drugs to treat CNS disorders
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Carninci, p. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning Methods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK015320 1232 bp mrNA HTC 05-JUL-2001 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930435C18, full insert sequence. AK015320 AK015320 GI:12853612
3 (bases 1 to 1232)
3 (bases 1 to 1232)
5hibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome research. 10 (10), 1617-1630 (2000)
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/db_xref="MGD:MGI:1907852"
/db_xref="MGD:MGI:1921906"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Mus musculus"
/strain-"C57BL/6J"
                                                                                                                                                                GALTFASKQESGNPTPSGWRIKGQCVATWLSLSASSPLQCKNTLASCLGRKTRSPSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                       /protein_id="BAB29795.1"
/protein_id="BAB29795.1"
/db_xref="G1:12853613"
/translation="MCHTSGTCMPTGLCSSSLSPPPPSIALSTTMTISALORTOPARS
                                                                                                                                                                                                                                                                           /codon_start-1
                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
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     /note∸"putative"
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/note="putative"
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                                                                                                                                     1 (bases 1 to 1376)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
99279253
                                                                                                                                                                                                                                                  Mus musculus (strain:c5/H1/6J) adult male testis clone_lib:RIKEN full-length enriched mouse cDNA l clone:4921507G06.
                                      Carninci, P., Shibata, Y., Hayatsu, N., Sngahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                     Mus musculus adult
                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                        library, clone:4921507G06, full insert sequence
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Pred. No. 2.9e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Encyclopedia Project of Genome Exploration Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to primer proper mouse tissues. First strand CDNA was primed with a primer proper primer and primer primer generated by using trehalose thermo-activated reverse transcriptase prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second and subsequently enriched for full-length by cap-trapper. Second Strand cDNA was prepared with the primer adapter of sequence [5' strand cDNA was prepared with the primer adapter of sequence [5' strand cDNA was prepared with the primer adapter of sequence [5' strand cDNA of size comprised longer than 7 kb was with BamHI and XhoI. CDNA of size comprised longer than 7 kb was with BamHI and XhoI. CDNA of size comprised longer than 7 kb was with BamHI and North Lambda FLC I. Cloning sites, 5' end: Sall; 3' bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3'
                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Arakawa, M., Rato, H., Kawai, J., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Imotani, K., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Kojina, Y., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Kojina, Y., Konno, H., Saito, R., Sokai, K., Saho, H., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, K., Saho, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409, 685-690 (2001)
5 (bases 1 to 1376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (GSU), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Functional annotation of a full-length mouse cDNA collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1376)
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27.3%;
milarity 67.1%;
Conservative
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/db_xref="MGD:MGI:1903273"
/db_xref="MGD:MGI:1918065"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                     /dev_stage="adult"
366 c 349 g
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                                                                                                                                                                                                                                                   /clone_lib="testis"
/clone_lib="KIKEN_full-length_enriched_mouse (DNA_library"
                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                            /clone="4921507G06"
             0;
         Score 230; DB 12;
pred. No. 3.1e-47;
0; Mismatches 160;
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Actinopteryali; Neopteryali; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryali; Percomorpha; Tetraodontiformes;
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Vector: pBlueScript II KS
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                                                                                                                                 One pass dye-terminator sequencing of cosmid cloned genomic
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υ.
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              /organism-"Takifuqu rubripes"
/db_xref."taxon:31033"
/clone_lib-"cosmid_015G16"
/clone="015G16aA10"
/clone="015G16aA10"
                                                                                                        Location/Qualifiers
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clone 015G16aAlO g
                                                                                                                                                                                                                 C Human Genome Mapping Project Resource CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
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Score 177.2;

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Length 619;

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AZ949429
BOAL STANDARD CSS
AZY-APK ZOUT
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BOAL STANDARD CSS AZY-APK ZOUT
BOAL CLORE UNGCZMOZIJZJ R. DNA sequence.
AZ949429
AZ949429
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                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: |
Plate: 0212 row: J column: 23
Seq primer: CACA/AGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus muscutlus
Eukaryota; Metazoa; Chordata; Craniat; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 616)
                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid inserts
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                                                                                                                                                                                             High quality sequence stop: 616.
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801 585 7177
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/lab_host="E, coli strain XL10-Gold, Thresistant, F-"
/note="Vector: PWD42Nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                               /db_xref."taxon:10090"
/clone="uugc2M0212J23"
/clone_lib="Mouse 10kb plasmid uugc2M library"
                                                                                                                               /organism-"Mus musculus"
/strain-"C57BL/6J"
                                                                                                                                                                               Location/Qualifiers
                                                                   /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:13820656
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source
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                                                   Clones are derived from the mouse BAC library RPC1-24. For BAC library availability, please contact Pieter de Jong (pdejondemail.cho.ord). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC epage: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 257 row: G column: 14 Seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegayo, G., Geer, K., Kroll, M., Shvartsbeyn, A.,
Knssell, D., de Jond, P., and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Other_GSSs: RPC1-24-257G14.TV
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Mammalia: Eutheria: Redeutia:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse BAC End Sequences from Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA se juence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases t to /io)
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301 838 0208
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pred. No. 4.8e-27;
0; Mismatches 0;
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Sciuroqnathi; Muridae; Murinae; Mus
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x88325
                                                                                                                                                                      Direct Submission
Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of Medical Genetics, University and Cantonal Hospital of Geneva, Medical Hospital of Geneva, SWITZERLAND
1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
3 (hases 1 to 147)
Chen, H., Chrast, R., Rossier, C., Morris, M.A., Lalioti, M.D. and Antonarakis, S.E.
Cloning of 559 potential exons of genes of human chromosome 21
                                                                                                                                                                                                                                                                                                                    Chen,H.M., Rossier,C., Chrast,R. and Antonarakis,S.E. Cloning of trapped exons from human chromosome 21 unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H.sapiens DNA
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Antonarakis, S.E.
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                             exon trapping Genome Res. 6 (8), 747-760 (1996)
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/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note-"Vector: pTARBAC1; Site_1: BamH1; Fire de Jong. The
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
Library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male c57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RPCI-24-257G14"
/clone_lib="RPCI-24"
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/strain="C57BL/6J"
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                  /note="trapped exon' 33 c 39 g
                                             /chromosome="21"
1. .147
                                                                       /db_xref~"taxon:9606"
                                                                                                     Location/Qualifiers
1. .147
                                                                                       /organism="Homo sapiens"
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AL236602
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Tetraodonidae, Tetraodon.

1 (bases | to 535)

Roest-Crollius H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouncau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-APR 2000) to the EMHL/GenHank/DDBJ databases Submitted (12-APR 2000) to the EMHL/GenHank/DDBJ databases This sequence is a simple read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weissenbach, J. Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
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Tetraodon nigroviridis DNA sequence
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                                                                                                                      Score 126.6; DB
Pred. No. 1.9e-21
5; Mismatches 7
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1 (bases 1 to 450)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (DISORDER), Tumor Gene Index (DISORDER)
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Email: cyapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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Insert Length: 753 Std Error: 0.00
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BNA Sequencing by: Washington University Genome Sequencing Center DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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15; Conservative
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Tetraodon nigroviridis genome survey sequence T7
035E22 of library G from Tetraodon nigroviridis,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Euteleostei; Neoteleostei;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL249234.1 GI:7970246
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cms.fr/Tetraodon.
                                                                                                                                                                                                                                                         Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                        Tetraodontidae: Tetraodon
1 (bases 1 to 1086)
                                                                                                                                         Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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AL205171.1 GI:7863990
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Tetraodon nigroviridis.
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Tetraodon nigroviridis genome survey sequence T7
151K15 of library G from Tetraodon nigroviridis,
                                                                                                                                      Submitted (12-APR-2000) to the EMBI/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovigenome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon nigroviridis Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostei Actinopterygii; Neoteleostei Percomorpha; Tetraodontiformes; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                               Human gene number estimate
                                                                                                                                                                                                                                                                                                                             Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                                                                                                                                                                                                                                                                                                                                                               Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                            Weissenbach, J. Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodontidae; Tetraodon.
1 (bases 1 to 1068)
Roest-Crollius,H., Jaillon,O.,
Bouneau,L., Billault,A., Queti
                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                       Genoscope.
                                                                                                                                                                                                                                                                   Unpublished
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/note="Genoscope sequence
/326 c 323 g 187
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/organism-"Tetraodon nigroviridis"
/db_xref."taxon:99883"
/clone="035E22"
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              /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="151K15"
/clone="151K15"
/clone="151K15"
clone="Genoscope sequence ID : COAG151ArO8LP1-end : 269 c 296 g 257 t 6 others
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Quetier,F., Saurin,W., Hernot
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Best Local Similarity
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Tetraodon nigroviridis genome survey sequence T7 end of clone
140F02 of library G from Tetraodon nigroviridis, genomic survey
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Roest-Crollins, H., Jaillon, O., Dasilva, C., Fizames, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS; genome survey sequence.
Tetraodon nigroviridis.
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AL198405.1 GI:7836556
                                                                                                                                                                                                        Direct Submission
Submitted (12-APK-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of
scale clone-end sequencing project of the Tetraodon nigrov
genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 862)
Roest-Crollins, H., Jaillon, O., basilva, C., Boune
Roest-Crollins, H., Jaillon, O., basilva, C., Boune
Hernot, A., Fizames, C., Wincker, P., Brottier, P.,
Sanrin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charaterization and repeat analysis of the or freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                               Genoscope.
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                        a
          /clone-
/clone_lib="G"
/note="Genoscope sequence
/note="Genoscope sequence
154 c 204 g 212
                                                                            /organism=""etraodon nigroviridis"
/db_xref="taxon:99883"
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Pred. No. 5.4e-11;
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23 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compact genome of the
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,A. and
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DB 13;

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AL191311 G1:7829415
AL191311.1 G1:7829415
GSS; genome survey sequence.
Tetraodon nigroviridis.
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                              CNS02CLY 611 bp DNA GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 255N21 of library G from Tetraodon nigroviridis, genomic survey
gtgtltgcaagcacateggggacyclygtyccclycccyqetycayycalccclcclqtq 266
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1 (bases 1 to 611)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                           102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryot: Metazoa; Chordata; Cranial: Vertebiata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontliformes;
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Bernot,A., Fizames,C., Wincker,P.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2000) to the EMBL/GenHank/DDBJ databases this sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodom nigroviridis genome. For more information, please take a look at http://www.genoscope.cms.fr/Tetraodom.
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                                                                                                                                                                                    109
                                                                                            Conservative
                                                                                                                                                                                                            /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="255N21"
/clone=[ib="G"
/note="Genoscope sequence ID : COAG255CG11SP1-end
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67.5%;
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                                                                                              Score 69; DB 13; Length 611; pred. No. 5.7e-07; 5; Mismatches 43; Indels
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p., Brottier,P., Quetier,F.,
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Tetraodon nigroviridis
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AL295695
AL295695.1 GI:8034275
GACTETETET 133
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1 (bases 1 to 656)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neobteleostei; Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
                           gactutteut 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide Tetrackon ingroviridis DNA sequence Unpublished 3 (bases 1 to 656)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission submission to the EMBL/GenBank/DDBJ databases submitted (12-Apk 2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a language connected sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizzmes,C., Wincker,P., Brottler,P., Quetler,F.,
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Similarity 69.2%;
90; Conservative
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/Ah xref "taxon:99884"
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sequence.
AL292982.1 GI:8031562
GSS; genome survey sequence.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostei;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; TetraodonLiformes;
Tetraodontidae; Tetraodon.

CE 1 (bases 1 to 691)
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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blobelp@lymp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
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AL027078.1 G1:326421
GSS; genome survey sequence.
GSS; genome survey sequence.
Takifugu rubripes
Takifugu Teleostel; Butelcostel; Neotelcostel;
Acanthomorpha; Acanthopterygii; Percomorpha; Telraodontiformes;
Acanthomorpha; Acanthopterygii; Percomorpha; Telraodontiformes;
Takifugu
Telraodontidae; Takifugu
Telgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
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/db_xref="taxon:31033"
/clone_lib="cosmid 096F20"
/clone="096F20bG4"
/clone="096F20bG4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (12-APK-2000) to the
This sequence is a single read
                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraddon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
3 (bases l
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                                                                                                                                                                                                                                                                                                                                                                                                                                  genome. For more information, presse characterization and the http://www.denoscope.cms.fr/Tetraodon.
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milarity 82.9%;
Conservative
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/db_xref-"laxon:99883"
/clone-"113J17"
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/clone_lib-"G"
/note-"Genoscope sequence ID : COBG113CEO9LP1-end :
/note-"Genoscope sequence ID : COBG113CEO9LP1-end :
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                     nucleic search, using sw model
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| (cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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| (cgn2_6/ptodata/2/ina/6A_COMB.seq:*
| (cgn2_6/ptodata/2/ina/6B_COMB.seq:*
| (cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
| (cgn2_6/ptodata/2/ina/backfiles1.seq:*
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 DВ
                     US-08-752-3078-6
US-08-752-3078-6
US-08-690-473-1
US-09-259-821A-1
US-08-48-659-1
US-08-48-659-1
US-08-459-850-32
US-08-459-850-32
US-08-459-850-9
US-08-034-650-9
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US-08-333-9564-1
US-08-334-958-2
US-08-334-958-2
US-08-334-2578-4
US-08-335-2578-4
US-08-884-599-2
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Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 24, Appli
Sequence 9, Appli
Sequence 17, Appli
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Best Local Similarity 65.1%;
Matches 501; Conservative
                                                                                                                                 Sequence 1, Application US/08690473 Patent No. 587692
                                                                                                                        GENERAL
                                                            APPLICANT: Leopardi, I
APPLICANT: ROIZMAN, B
APPLICANT: ROIZMAN, B
TITLE OF INVENTION: HI
TITLE OF INVENTION: II
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 ACTCTTACACAAAGCCCGCCCTGAAGATGTTGGCACCAGCCTCTACTTTGTAAATGACT 189
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                                                  CORRESPONDENCE ADDRESS:
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ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STAFF: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCCCCCAGUGCGGCCCTTCGATGGTACCTGGCCACAGGGGACGACATCTACGACGTGC 309
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                                                                                                                                                                                                       GCTTCCACTCCCAGGAAGTGTGGGCCGGCCACACCGTGGAGCTGCCCTGC 839
                                                                                                                                                                                                                                                    GCAATGGGGCACGCCTCTCTGTGACAGACCCTGCTGAGTCGATCCCCACCATCCTGGATG
                                                                                                                        INFORMATION:
                                                                          HERPES SIMPLEX VIRUS 1CP4 AS INHIBITOR OF APOPTOSIS
                                                                                                    Bernard
                                                                                                               Rosario
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US-09-259-821A-1/c
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                                                                                                                                                                                          ; TYPE: DNA ; ORGANISM: HERPES VIRUS, TYPE 1 US-09-259-821A-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                          Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.7%;
Best Local Similarity 62.0%;
Matches 62; Conservative
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CURRENT FILING DATE: 1994-03-01
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR EILING DATE: 1996-07-26
NUMBER OF SEO 1D NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 1
LENGTH: 4257
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09259821A
Patent No. 6210926
                                                                                                                    Matches
                                                                                                                               Query Match 4.7%;
Best Local Similarity 62.0%;
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LEOPARDI, ROSARIO
APPLICANT: ROIZMAN, HERNORU
TITLE OF INVENTION: HERDES SIMPLEX VIROS ICP4 IS
                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0
FILING DATE: 26-JUL-1996
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Highlander, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARTELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2229 CAGGCCCOUGCGCCTCCGCCTCCGGCGGCGCGGGGGGGGGGCCCGCGGGTCCCTCCGG 2170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 512/x--
TELEPHONE: 512/474-7577
TO TO NO:
2169 CCGCGGGGCTGGCGGCCCGGCCAGCCCGGG
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                                                      Highlander, Steven L
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                                                                                                                     Score 39.2; DB Pred. No. 0.066; 0; Mismatches
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US-08-843-659-1/c

Patent No. 6218103

GENERAL INFORMATION:

APPLICANT: Leopardi,
APPLICANT: Roizman,
TITLE OF INVENTION:
TITLE OF INVENTION:

Bernard Roasrio

HERPES SIMPLEX VIKUS US3 AND ICP4 AS INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433

Sequence 1, Application US/08843659

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ORGANISM: Herpes simplex virus
STRAIN: Herpes Simplex Virus Type 1
US-08-458-568A-11
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Sequence 32, Application US/08197792
Patent No. 5525488
                                                                                                                                                                                                                                                                                                                                                      RESULT
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin
NUMBER OF SEQUENCES: 44
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COMPUTER READABLE FORM:
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APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WORDPERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30.317
REFERENCE/POCKET NUMBER: DFF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                          COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12001 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                         STREET: 460 FOIL .-
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                 ADDRESSEE:
 FILING DATE:
              APPLICATION NUMBER:
                                                                                                                          94080
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                                                                                                                                                                                    E: Genentech, Inc.
460 Point San Bruno Blvd
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UMBER: US/08/197,792
16-FEB-1994
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; TOPOLOGY: linear US-08-843-659-1

0

TYPE: nucleic acid STRANDEDNESS: single

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs

ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:519

FILING DATE: CC CLASSIFICATION:

APPLICATION NUMBER: US/08/843,659

Concurrently Herewith

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURKENT APPLICATION DATA:

COMPUTER READABLE FORM:

COUNTRY:

Houston

Texas

United States

77210

MEDIUM TYPE: Floppy disk

듣 ş 5 US-08-458-568A-11 Sequence 11, Application US/08458568A Patent No. 5821339 Matches Query Match Best Local Similarity Matches 62; Conserv APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions an
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: GENERAL INFORMATION: 2169 ссассававаствасавьёссваесссваесливесливае 2130 62 egetgymtegetggetggeggggegggegggegggeggggggg STREET: One Liberty CITY: Philadelphia STATE: PA ADDRESSEE: 4.7%; nilarity 62.0%; Conservative E: Woodcock, Washburn, Kurtz, Mackiewicz & No. One Liberty Place, 46th floor Compositions and Methods for Treatment of Herpesvirus 0; Mismatches Score 39.2; DB 4; Length 4257; pred. No. 0.066; 8 Indels 5821339ris **:** Gaps

PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 08-OCT-

07/958414

CLASSIFICATION:

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Best Local Similarity
Matches 72; Conserv
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APPLICATION NUMBER: 07/215
FILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/906
FILING DATE: 31-DEC-1986
                                                                                                                                                                                                                                 GENERAL INFORMATION
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/74
FILING DATE: 12-AUG-1991
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APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
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APPLICATION NUMBER: 06/783910
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TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                            APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
TITLE OF INVENTION: Using such Nucleic Acid
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        1569 TCCTTTCTTCCTCCAGCATCGGAGTGGGGACAGCAGTTGCTCCAACGGGAATATTGTCCT 1628
                                                                                                                                                                                                                                                                                                                                               1629 CTCCTTT 1636
COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                       CORRESPONDENCE ADDRESS
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TELEX: 910/371-7168
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                                         ADDRESSEE:
STREET: 46
CITY: Sout
STATE: Cal
COUNTRY: U
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STRANDEDNESS: singl
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                               94080
                                                          T: 460 Point San Bruno Blvd
South San Francisco
California
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                                                                                                               Inc
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US-08-459-214-32
Sequence 32, Application US/08459214
Patent No. 5716810
GENERAL INFORMATION:
APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid E
TITLE OF INVENTION: Beta Chains of
TITLE OF INVENTION: Using such Nuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: US-08-459-850-32
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 12-AUG-
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APPLICATION NUMBER: 07/958414
FILING DATE: 08-0CT-1992
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APPLICATION NUMBER: (
FILING DATE: 03-OCT-1
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APPLICATION NUMBER:
FILING DATE: 07-FEB-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
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                                                                                                                                                                                                                                                                                           1569 TCCTTTCTTCCTCCAGCATCGGAGTGGGGACAGCAGTTGCTCCAACGGGAATATTGTCCT 1628
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                                                                                                                                                                                                                                                            122 ctccttgt 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 4.68;
Local Similarity 56.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: singio
                                                                                                                                                                                                                                                                                                              LENGTH:
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SYSTEM: PC-DOS/MS-DOS
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 Seeburg
Nucleic Acid Encoding the Alpha or
Nucleic Acid Encoding and Method for Synthesizing Polypept
Beta Chains of Inhibin and Method for Synthesizing Polypept
Using such Nucleic Acid
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CORRESPONDENCE ADDRESS:

Genentech,

STREET:

South San Francisco

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TOPOLOGY:
US-08-459-214-32
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RESULT 9
US-08-716-942-24
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
FILING DATE: 17-FEB-
PRIOR APPLICATION DATA:
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PAPPLICATION UNBER: 08-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
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APPLICATION NUMBER: 07/215466
FILING DATE: 05-JUL-1988
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APPLICATION NUMBER:
FILING DATE: 31-DEC-
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NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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TELEPHONE: 415/225-1896
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NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
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                                                                                                                                                                            APPLICATION NUMBER: 07/70 FILING DATE: 12-AUG-1991
                                                                                                                  1569 TCCTTTCTTCCTCCAGCATCGGAGTGGGGACAGCAGTTGCTCCAACGGGAATATTGTCCT 1628
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                                                         ||||||| |
| 1629 CTCCTTTT 1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                     122 ctccttgt 129
                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                      Local Similarity 56.2 nes 72; Conservative
                                                                                                                                    62 cgctqgctcgctqgctcgcgggaggccgqgcagcaggaggatgtqalactggctct 121
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56.2%;
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Sequence 24, patent No. 58
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US-08-716-942-24
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APPLICANT:
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Best Local Similarity 54.2%;
Matches 77; Conservative
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CURRENT APPLICATION DATA:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/004,157
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GCCAGCAGTTCGACATGGTCAC 293
                                             ACTTCGUGACTGAGGTCACCGGGAACATGATCAACAACTCGACGATCACGAACCTGGCAG 271
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SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD
COMPOSITIONS OBTAINED THEREBY
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Pred. No. 0.09;
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APPLICATION NUMBER: US 07/
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKUlis, Paul N.
REGISTRATION NUMBER: 16,77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 9:
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APPLICANT: VERRIPS, Cornelis T.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HEFFROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: doub
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TELEX: 6714627 CUSH
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1615 L. Street, N.W.
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Pred. No. 0.12;
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US-08-449-015-9
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ATTORNEY/AGENT INFORMATION:
NAME: KOKALIS, PAUL N.
REGISTRATION NUMHER: 16,773
REFERENCE/DOCKET NUMBER: PNK/5970/91731
TELECOMBUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 822-0944
TELEEX: 6714627 CUSH
TELEEX: 6714627 DISH
INFORMATION FOR SEQ ID NO: 9:
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Best Local Similarity
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APPLICANT: VERKLPS, Cornells T.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
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APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICATION NUMBER: US 07/727,235
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                                                   1806
                                                                                                                    1746 CCGCGGCAAGCGGCGGCGGCGGAAGGCCGCCATGCCGTTGCCGGGCGCGCTGCCGGGCGCGC 1805
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OPERATING SYSTEM: PC-NOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1615 L.: CITY: Washington
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COUNTRY: USA
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Pred. No. 0.12;
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US-09-244-796-17/c
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ARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
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Best Local S
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Patent No. 6258558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SZOSTAK, JACK W.
APPLICANT: Roberts, Richard W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT APPLICATION NUMBER: 05/035,963
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
SARLIER FILING DATE: 1997-01-27
SARLIER FILING DATE: 1997-01-27
                GENERAL INFORMATION:
APPLICANT: SZOSEAK, Jack W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(289)
OTHER INFORMATION: n - A,T,C or -09-007-005-17
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FILE
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REFERENCE:
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  00786/350007
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9.3%; Pred. No. 0.089;
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                                                RNA-PROTEIN
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; NAME/KEY: misc_feature
; LCCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or
US-09-244-796-17
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US-08-091-569-1/c
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/64,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08091569 Patent No. 5494792
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ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                         NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: Foley & Lardher
                                                                                                                                                                                                                                                               APPLICANT: KAMBOJ, Rajender
APPLICANT: NUTT, Stephen
APPLICANT: SHEKER, Lee
APPLICANT: WOSNICK, Michael
TITLE OF INVENTION: KAINATE-BINDING HUMAN CNS RECEPTORS
TITLE OF INVENTION: THE EAA2 FAMILY
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CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                             Suite 500
                       Version #1.25
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FILING DATE: CLASSIFICATION:

US 07/750,081

APPLICATION NUMBER:

US/08/091,569

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Best Local Similarity 53.1%;
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APPLICATION NUMBER: US 07/
FILING DATE: 27-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFORMATION FOR SEQ ID NO: 1:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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LENGTH: 3695 base pairs
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APPLICANT: NUTT, Stephen
APPLICANT: SHEKTER, Lee
APPLICANT: WGSNICK, Michael
TITLE OF INVENTION: KAINATE-BINDING HUMAN CNS RECEPTORS
TITLE OF INVENTION: THE EAA2 FAMILY
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COMPUTER READABLE FORM:
,MEDIUM TYPE: Floppy disk
,COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: double
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                                                                                            STREET: 1800 Diag
CITY: Alexandria
STATE: Virginia
                                                              COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                   INFORMATION:
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Search completed: March 4, 2002, 05:12:23 Job time: 16997 sec
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Best Local Similarity 53.1%;
Matches 78; Conservative
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INFORMATION FOR SEU 1D NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/203,676
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 27-AUG-1991
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                                                                        2987 GCCGCACTCCTGGCAGACGCCACCT 2961
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                                                                                                   122 etecttqttecaqagettegegaatgt 148
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STRANDEDNESS: double
TOPOLOGY: linear
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TELEFAX: (703)683-4109
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176. 229
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SOURCE ORGANISM REFERENCE KEYWORDS VERSION ACCESSION COMMENT AUTHORS JOURNAL RS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci RS Konno, H., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, J., Ishikawa, T., Itoh, M., Hirozane, T., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Shibata, K., Shibata, K., Shigemoto, Y., Saito, H., Sakai, C., Sato, K., Shibata, K., Shigemoto, Y., Sunayawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Y., Sugahara, Y., Yanoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, Y., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., RIKEN Mouse ESTS (Konno, H., et al.) BB336040 279 bp mRNA EST 11-JUL-2000 BB336040 RTKEN full-length enriched, 10 days neonate medulla oblongata Mus musculus cDNA clone B830046F24 3′ similar to AF217525 Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule (DSCAM) mRNA, mRNA sequence. Unpublished (2000)
Contact: Yoshihide Hayashizaki
Caboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Musidaes: 1 to 279) 53 BB336040.1 G1:9844803 вн 336040 nouse mouse. 22 Suehiro-cho, 81-45-503-9222 230-0045, Japan Murinae; Mus.

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FEATURES
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Carninci.p., Nishiyama.Y., Westover, A., Itoh, M., Nagaoka,S., Sasaki
Carninci.p., Nishiyama.Y., Westover, A., Itoh, M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
System. Genome Res. 9 (5), 463-470 (1999)
System. Genome Res. 9 (5), 463-470 (1999)
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/dev_stage="10 days neonate"
/lab_host="DH10B"
/note="Site_1: Sal1; Site_2: BamHI; cDNA library was
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Al. Unpublished (2000)

Al. Orditact: Yoshihida (Hayashizaki)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
Fax: 81-45-503-9226
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Carninci,P. Nishiyama,Y. westover,A. Itoh,M., Nagaoka,S., Sasaki
Carninci,P. Nishiyama,Y. Mestover,A. Itoh,M., Kitsunai,T. Akiyama,J., Shibata,F., Muramatsu,M., Okazaki
Temmaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Temmaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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//issue_type="medulla oblongata"

//issue_type="medulla oblongata"

//dev_staue="10 days neonate"

//ab_bost="0bHOB"

//ab_bos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Mus musculus"
contributed to prepare mouse tissues. 1st strand primed with a primer (5^\prime)
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RESULT 3
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 cactgtcatagcctgtgatqgggctgttgccatcaaaccccatggtccacctgagcgtga 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tygtgcgagcittgacatctcttgatctcaatctcggggaggatctggggggttcttgcact 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtgagttgaaltattccacqgtcctccccgtatgaattgatagcatqgcagqagaagaaa 626
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BB381728
BB381728.1
                                                                                                                                              Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara C., Kusakabe, M. Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Ola, H., Okazaki, Y., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, K., Shipamoto, Y., Shiqagawa, A., Shiraki, T., Sogabe, Y., Sugaliara, Y., Suzuki, H., Tayawa, A., Tak. ashi, F., Tominada, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamanura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Riken Mouse Ests (Konno, H., et. al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB381728 252 bp mRNA EST BB381728 RIKEN full-length enriched, 0 day neonate cerebellum Mus BB381728 RIKEN full-length enriched, 0 day neonate cerebellum Mus musculus cDNA clone C230015109 3' similar to AF2175_5 Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule (DSCAM) mRNA, mRNA
                                                                                                                                                                                                                                                                                                                                                      Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Cari, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Ito Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciuroquathi; 1 (bases 1 to 252)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Veriebrata; Euteleostomi;
                Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanadawa 230-
                                                                                 Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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Pred. No. 7.7e-53;
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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cDNA. Proc. Natl. Arad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further details
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                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Genome Science Caboratory in Riken Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified pBluescript KS(+) after bulk excision from Lambda FLC 1. ^{\rm s} _{\rm 3} _{\rm 7} i.c. _{\rm 57} g _{\rm 53} t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="0 day neonate"
/lab_host="pH10B"
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/clone="C230015109"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /missue_type-"cerebellum"
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Pred. No. 2.5
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No. 2.5e-51;
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RESULT 4
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Al Unpublished (2000)

Al Contact: Yoshidae Hayashizaki
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BB336019 RIKEN full-length enriched, 10 days neonate medulla
oblongata Mus musculus CDNA clone B830046C02 3′ similar to AF217525
Homo sapiens clone cDSCl Down syndrome cell adhesion molecule
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Bmail: genome-gsc.riken.go.jp,

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki

N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by

Thermostabilization and thermoactivation of rull length

trehalose and its application for the synthesis of rull length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), S20-524 (1998)

Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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//lab_host="DH10B"
//note="Site_1: Sal1; Site_2: BamHI; cDNA library was
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//note="Site_1: Sal1; Site_2: BamHI; cDNA library was
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//note="Site_2: BamHI
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/tissue_type="medulla oblongata"
/dev_stage="10 days neonate"
prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                   /clone="B830046C02"
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                                                                                 P. Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kayawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Izawa,M., Kadota,K., Kayawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Kiyosawa,H., Kojima,Y., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Matsuyama,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,
Y., Shiqamaya,A., Takahashi,F., Tominaga,N., Toya,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,
Yano,R., Yasunishi,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Konno,H., et al.)
Contact: Yoshihide Hayashizaki
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Email: genome-res@gsc.riken.go.jp,

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Carninci,P., Nishiyama,Y., Westover,A., ILoh,M., Naqaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Thomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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/clone_lib="RIKEN full-length enriched, 10 days neonate
medulla oblongata"
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BH461534 RIKEN full-length enriched, 12 days embryo spinal ganglion
Mus musculus cDNA clone D130072G13 3′ similar to AF217525 Homo
sapiens clone cDSC1 Down syndrome cell adhesion molecule (DSCAM)
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UKU:http://qenome-asc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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trehalose and its application for the synthesis of full length
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cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), S20-524 (1998)
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
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1-7-22 Suethiro cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Mammalia; Entheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Carpinel, P. and Hayashizaki, Y.
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     /tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
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12 Konno, H. Aizawa, K. Akahira, S., Akiyuma, J., Arakawa, T., Carninci K. Konno, H. Aizawa, K. Akahira, S., Akiyuma, J., Hayatsu, N., P. Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P. Endo, T., Fukuda, S., Fukunishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., P. Endo, T., Kadola, K., Sayawa, I., Kaj, C., Kawai, J., Kikuchi, N., Izawa, M., Kadola, K., Kagawa, I., Kaj, C., Kawai, J., Kikuchi, N., Kayawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Sugahara, Y., Y., Shinagawa, A., Shiraki, T., Soqabe, Y., Sugahara, Y., Y., Shinagawa, A., Shiraki, T., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, T., Yoshida, K., Yoshiki, A., Yoshino, M., Suzuki, H., Tagawa, A., Shiraki, Y., Yoshida, K., Yoshiki, A., Yoshino, M., Suzuki, H., Tagawa, A., Shiraki, Y., Yoshida, K., Yoshid
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Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Email: genome-res@gsc.riken.qo.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,p., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S.,,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Carninci,P. and Hayashizaki,Y. Cloning. Methods Enzymol. 303.
TGGTGCGAGCTTTGAAANTCT-TTGATCTCAATCTCGGGAGGATCTGGGGGGTTCTTGCACT 124
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/dev_stage="6 days neonate"
/lab_host="bH10H"
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URU:http://genome.gsc.riken.go.jp,
URU:http://genome.gsc.riken.go.jp,
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
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Thermostabilization and thermoactivation of thermolabile enzymes by
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Thermostabilization and thermoactivation of the so, thesis of full length
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cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Tohan, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tohan, M., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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The Institute of physical and Chemical Research (RIVEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa (0-0045, Jap
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Konno, H., Akadura, S., Fukunishi, Y., Hara, A., Hayatay, N., P., Endo, T., Pukunia, S., Fukunishi, Y., Hara, A., Hayatay, N., P., Endo, T., Pukunia, S., Fukunishi, Y., Hara, A., Hayatay, N., Hara, J., Kuriha, T., Itoh, M., Hara, Y., Kurihara, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, K., Mizuno, Y., Nator, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, Y., Watanaba, T., Sato, K., Shibata, Y., Sugahara, Y., Y., Shiyemoto, Y., Saito, H., Tayawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, Yasunishiki, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, Yasunishiki, A., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehitro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehitro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehitro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-25 Suehitro-cho, Tsurumi-ku, Yok
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BB330426 KIKEN tull-length enriched, 6 days neonate medulla objunyata Mus musculus cDNA clone B730013K15 3' similar to AF217525 Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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BB330426.1
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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Pred. No. 3e-47;
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Carninci,P. and Hayashizaki,Y...
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ILOh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., and Hayashizaki,Y.
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                                                              BB331552 253 bp mRNA EST 11-JUL-2000
BB331552 RIKEN full-length enriched, 6 days neonate medulla
oblongata Mus musculus CDNA clone 8730035G02 3′ similar to AF217525
Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule
                     вв331552
                                             (DSCAM) mRNA, mRNA sequence.
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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medulla oblongata"
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998).
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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Fax: 81-45-503-9216
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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/db xret "taxon:10090"
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                                                                                                                                                                                                                                                                  contributed to prepare mouse tissues. 1st strand cDNA
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BB280255 KIKEN full-length enriched, adult retina Mus musculus cDNA
clone A930024N03 3' similar to AF217525 Homo sapiens clone cDSC1
Down Syndrome cell adhesion molecule (DSCAM) mKNA, mKNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanayawa 230-0045, Jap Tel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
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URJ:http://genome.gsc.riken.go.jp,
URJ:http://genome.gsc.riken.go.jp,
Carninci,P, Nestover,A., Itoh,M., Nagaoka,S., Sasaki
Trehalose and its application for the synthesis of full length
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Toh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Toh,M., Kitsunai,T., Akiyama,J., Shibata,K., Muramatsu,M., Okazaki
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 81-45-503-9216

    and Hayashizaki, Y.
    automated filtration-based high-throughput plasmid preparation

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Carnincl, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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BB333910 286 bp mRNA EST 11-JUL-2000
BB333910 RIKEN full-length enriched, 10 days neonate medulla
BB333910 RIKEN full-length enriched, 10 days neonate medulla
oblongata Mus musculus cDNA clone BB30016017 3' similar to AF217525
HOMO Sapiens clone cDSC1 Down syndrome cell adhesion molecule
(DSCAM) mRNA, mRNA sequence.
BB333910
BB333910.1 GI:9042673
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nilarity 25. 5;
Conservative
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/tissuc_type="retina"
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KONNO, H., AÍZAWA, K., AKANİIRA, S., AKİYAMA, J., ISAKAWA, T., CARNÎNCÎ

P., ENDO, T., FUKUDÂ, S., FUKUNİSHİ, Y., HATA, A., HAYALSU, N.,

P., ENDO, T., FUKUDÂ, S., FUKUNİSHİ, Y., ISAİKAWA, T., İLOH, M.,

HİROZANE, T., HORÎ, F., ISHİİ, Y., ISAİKAWA, J., ISAİKAWA, T., İLOH, M.,

IZAWA, M., KADOCE, K., KAQAWA, I., KALİ, C., KAWAİ, J., KİKUCHİ, N.,

KİYOSAWA, H., KOİIMA, Y., KONDO, S., KOYA, S., KURİHATA, C., KUSAKAİ, Y.,

MALSUYAMA, T., MİKLİ, R., MİZUNDO, Y., NAKAMURA, M., ODA, H., OKAZAKİ, Y.,

MALSUYAMA, M., SAKAİ, C., SƏLO, K., ShİDALA, K., SHİDALA,

ONO, T., OWA, C., SAİLO, H., SAKAİ, C., SƏLO, K., SHİDALA, K., SHİDALA,

Y., SHİYYAMA, A., TAKAHASHİ, F., TOMİNAYA, N., YOYA

SUZUKİ, H., SUZUKİ, H., TAQAWA, A., TAKAHASHİ, F., TOMİNAYA, N., TOYA

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YANDA, YASUMİ, H., TAQAWA, A., TAKAHASHİ, F., TOMİNAYA, YONAHARA, Y.,

YANDA, YASUMİ, H., TAQAWA, A., TAKAHASHİ, F., TOMİNAYA, N., YOYA

N., WATAMATIKA, YASUMİ, A., YOKOLA, T., YONAHARA, Y., YONAHARA, Y.,

N., WATAMATIKA, YASUMİ, YASUMİ, Y., YONAHARA, Y., YONAHARA, Y., YONAHARA, Y.,

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URL:http://genome.gsc.riken.go.jp/
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Similarity 83.3%;
95; Conservative
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BB331669 RIKEN full-length enriched, 6 days neonate medulla
oblongata Mus musculus cDNA clone B730037M12 3', similar to AF217525
Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule
(DSCAM) mRNA, mRNA sequence.
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Eukaryota: Metazoa: Chordata:
Mammalia: Eutheria: Rodentia:
1 (bases 1 to 280)
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jappels 81-45-503-9222
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pred. No. 4.8e-42;
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Schurognathi; Muridae; Murinae; Mus
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                                                                                                                                                            626
                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki

Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki

N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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                                                                                            further details
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/dev_stage="6 days neonate"
/lab_bust="DH10B"
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/clone="H730037M12"
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Pred. No. 9.9e-42;
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VERSION
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Qontact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., MuramatSu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trohalose and its application for the synthesis of full length
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Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y., Ozawa,Y., and Hayashizaki,Y.
and Hayashizaki,Y.
Carninci,P. and Hayashizaki,Y.
Carninci,P. and Hayashizaki,Y.
Land, Carninci,P. and Hayashizaki,Y.
Carninci,P. and Hayashizaki,Y.
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BB334670
BB334670.1 GI:9043433
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Tel: 81-45-503-9222
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                       contributed to prepare mouse tissues. Ist strand cDNA was primed with a primer (5' GAGAGAGAGGAGGAGCTCATT' TTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                       prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/tissue_type="medulia oblongata"
/dev_stage="10 days neonate"
/lab_host="DH10B"
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/db_xref-"taxon:10090"
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                                                             567 ytgayttyaattatteearqqieeleecegtatyaattyataycatgycaggagagaaa 626
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           coggaatetteteteaetq11qgcaaaatetgcagcgtagatat 670
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This cDNA sequence comprises the middle region of a cDNA clone comparises of the Ig superfamily with homology to CC member of a novel subclass of the Ig superfamily with homology to CC neural cell adhesion molecules. The 5' region (see AAV1985) cc and 3' region (see AAV1995) of the clone are also provided. The CC murine DS-CAM clone was isolated from a C57 Black/6 mouse brain CC cDNA library using human DS-CAM cDNA (see AAV1981) and AAV1988) as CC cDNA library using human DS-CAM cDNA (see AAV1988) as CC cDNA comparison vectors and host cells. The invention also provides human DS-CAM proteins (see CC probe. The invention also provides human DS-CAM proteins (see CC probe. The invention also provides human DS-CAM proteins (see CC probe. The invention also provides human DS-CAM proteins useful CC transgenic animals, antisense oligonucleotides, and primers useful CC mapplification of DS-CAM nucleic acids. DS-CAM polypeptides are associated with developmental and neurological processes. They can compare the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compared to the compa
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This cDNA clone codes for Down syndrome-cell adhesion molecule CC DS-CAM2 (see AAW42087), an extracellular, soluble protein belonging CC to a novel subclass of the 1g superfamily with highest homology to CC to anovel subclass of the 1g superfamily with highest homology to CC technique was applied to bacterial and P1 artificial chromosomes CC technique was applied to bacterial and P1 artificial chromosomes CC between ETS2 and MX1 by using cDNA from trisomy 21 human foetal CC brain. A unique cDNA fragment, designated E51 (see AAV31982), was CC brained and used to screen a trisomy 21 human foetal brain (14-wk CC obtained and used to screen a trisomy 21 human foetal brain (14-wk CC gestation) cDNA library. Further clones were obtained by exon CC trapping, and the complete DS-CAM2 cDNA sequence was identified. CC DS-CAM2 is a splice variant of membrane-bound DS-CAM1 (see AAW42086) and is deleted for the entire transmembrane domain. The DS-CAM come spans 900-1200 kb of genomic DNA and maps of thromosome
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signal transduction; trisomy 21; mental retardation;
holoprosencephaly; corpus (allosum agenesis;
schizencephaly; diagnosis; assay; human; ds; ss.
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CC 21q22.2-22.3. The invention also provides murine US-CAM partial CC sequences (see AAV31985-87), expression vectors and host cells, cells ransgenic animals, antisense oligonucleotides, and primers useful CC for amplification of DS-CAM nucleic acid. DS-CAM polypeptides are CC associated with developmental and neurological processes. They can CC methods of repairing (regenerating) damaged or severed peripheral CC methods of repairing (regenerating) damaged or severed peripheral CC nerves. The products can also be used in detection, diagnossis and CC therapy of developmental and neurological abnormalities such as CC therapy of developmental and neurological abnormalities such as the corpus callosum, or schizencephaly. Antisense oligonucleotides are used for inhibiting translation of mRNA.
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                           CC DS-CAM1 (see AAM42086), a cell surface glycoprotein belonging to a convel subclass of the 1g superiamity with highest homology to convel subclass of the 1g superiamity with highest homology to convel subclass of the 1g superiamity with highest homology to cell adhesion molecules. A modified direct cDNA selection cc technique was applied to bacterial and plantified chromosomes converged and MX1 by using cDNA from trisomy 21 human foetal contains and used to screen a trisomy 21 human foetal brain (14-wk cotained and used to screen a trisomy 21 human foetal brain (14-wk cotained and used to screen a trisomy 21 human foetal brain (14-wk cotained and used to screen a trisomy 21 human foetal brain (14-wk cotained and used to screen a trisomy 21 human foetal brain (14-wk cotained and used to screen a trisomy 21 human foetal brain (14-wk cotained and used to screen a trisomy 21 human foetal brain (14-wk cotained and used to screen a trisomy 21 human foetal brain (14-wk cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by exon cotained by e
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       2.3 The invention also provides murine DS-CAM (see AAV31985-87), expression vectors and host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6604 BP; 1673 A; 1827 C; 1768
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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful configuration of the invention may be used to treat diseases of the peripheral nervous containing a polypeptide or polynucleotide contained the peripheral nervous injuries, peripheral neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and contrained neuropathy and system disease, such as a local sease, amyotrophic contrained neuropathy and shy-Drager Syndrome. Other uses include the cutilisation of the activity chemotactic/chemokinetic activity, haemostatic activiny, inhibin activity, chemotactic/chemokinetic activity, haemostatic contrained neuropathy and therappy, drug screening, and thrombolytic activity, cancer diagnosis and therappy drug screening, and thrombolytic activity, arthritis and inflammation, leukaemias and contrained neuropathy activity, arthritis and inflammation, leukaemias and contrained neuropathy activity, arthritis and inflammation activity chemotactivity arthritis and inflammation.
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25-APR-2000;
09-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI58196 standard;
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypoptides, useful such as central nervous system injuries .
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Goodrich K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cgtgatgqtgatctcgttgctgggctcactcttgccaalccggttctttqqcgtacatgcg 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAGGTCACTGGCTGCAAGGTAACATCCATGGGGGGCCCATGGGGAGGGGCCTCCTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agatyagytggyttocaagtgaacttoc-tgagytgyanatnacyagotgoctoatcogc 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGCTGTACACAGATGCCGGGTGCAAGTCCACAATGTTGGCCTGGTTGATGGTGGGGGA 2483
                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGGCGATGGCCATGACGCGGTCAGGGTCGATGACTGTGTCTCCCCCTTCTCCCA
                                                                                                                                                                                              gytggatacayla-----cyggccartttcayqyttaatyatcctgtctctrttct-cca
                                                                                                                                                                                                                              GTCCCCACGGTCAGCGGCTTGAGCTTCAGTGTGGAGACGACCTCGTCGCCGTTGTCCTT
                                                                                                                                                                                                                                         atotictotoactgtlggcaaaatctgcaqcgtaqalateacttecteteceacetecil
                                                                                                                                                                                                                                                                         TTGGATCAAGCCCCGGTCCTCCCCCATACGAGTTGATGGCATGGCAGCTGAAGAACACAGA
                                                                                                                                                                                                                                                                                  ttgaattatteewegyteeteeegtatgaattyatayeatggeaygayaaaaaeeeyya 631
                                                                                                                                                                                                                                                                                                                   COGGCCTTCACCTC-CCGGATCTCCAGCTCTGGGGGGGGTCGGGGGGCTCTTGCACAGTGAG
                                                                                                                                                                                                                                                                                                                             cqagctttgacatctcttgatctcaatctcqqgaggatctgqgggttcttgcactqtuaq
                                                                                                                                                                                                                                                                                                                                                              TCGAAGCCCGTGATGATGCTGTTCCCGTCGAATCGCTGGGTCCAGCGCAGGTTCATGCTC
                                                                                                                                                                                                                                                                                                                                                                        gcgyacaatgatyggc 761
                                                                                                                                           GCGGATGATGATGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                            (first entry)
  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.38;
                                                                                                                                               2110
   immunomodulatory; antisclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244.8; 1/6 -
No. 1.1e-66;
No. 1.re-ches 237; Indels
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NO:
                             <del>-</del>8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2663
                                                                                                                                                                                                                                                                                                                            2306
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                                                                                                                                                                                                                                       2186
                                                                                                                                                                                                                                                                                  2246
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                                                                                                                                                                                             2126
                                                                                                                                                                                                                                                            691
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The present sequence encodes one of 32 movel human secreted polypeptides. CC The nucleic acid molecules and polypeptides they encode may be used in CC the prevention, diagnosis and treatment of diseases such as CC immune disorders (e.g. mulliple sclerosis, systemic lupus erythematosus CC and human immuno-deficiency virus (HIV) infections), hyperproliferative CC and human immuno-deficiency virus (HIV) infections), hyperproliferative CC (e.g. Scimitar syndrome, Claya's cardiomyopathy and coronary CC (e.g. Scimitar syndrome, Claya's cardiomyopathy and coronary CC (e.g. Huntington's chorea Alzheimer's disease and parkinson's disease), CC (e.g. Huntington's chorea Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, CC (e.g. Huntington's chorea, CC (e.g. Huntington's chorea, CC (e.g. Huntington's chorea, CC (e.g. Huntington's chorea, CC (e.g. Huntington's chorea, CC (e.g. Huntington's chorea, CC (e.g. Huntington's chorea, CC (e.g. Huntington's chorea, CC (e.g. Huntington's chorea, CC (e.g. Huntington's chorea, CC (e.g. Hunting
  AAT60757/C
ID AAT607
XX
AC AAT607
XX
DT 16-OCT
XX
DE Human
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                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.88:
Best Local Similarity 60.9%:
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological; antiinflammatory; anti-HIV; cytostatic; cardiant; vascular; anti-anglogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; antialzheimers; antiparkinsonian; antimicrobial; vulnerary; vaccine; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein coordinate data; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200121658-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 4: 890pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ni J, Baker KP, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SOL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5720 BP; 1293 A; 1677 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                their expression and activity.
Human aorti
                                                                                              AAT60757;
                                                                                                                                             AAT60757 standard;
                                                                                                                                                                                                                                                           16-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                   551 tgqgyqtictiqcaciqiqaqttyaaliattccgcqgtcctccccgtatgaattgatagc 610
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                                                                                                                                                                                                                                                                                                                                                       TGGCTTTTCCTGCTAATCTGACGGCAATGGAGACAGAGTCGTATCCCAAGGCATTGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000MO-0826013.
  preferentially expressed gene 1.
                                                 (first
                                                      entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 22;
Pred. No. 0.0057;
0; Mismatches 4!
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Rosen CA, Ruben
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SA, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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RESULT 7
AAZ51043/c
ID AAZ510
XX AZ510
AC AAZ510
XX DT 05-JUN
XX Human
DE Human
XX Human;
XX Human;
XX Human;
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                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                         ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; aortic preferentially expressed gene; APEG-1; aorta; specific; inhibition; growth; smooth; muscle; cell; vascular; proliferation; artery; restenosis; atherosclerosis; transplant; diabetes; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes the human aortic preferentially expressed gene 1 (APEG-1) polypeptide, which is aorta specific and inhibits the growth of smooth muscle cells. The APEG-1 polypeptide can be used to inhibit vascular smooth muscle cell proliferation in an animal via its introduction into an artery of the animal. In an animal via its introduction into an artery of the animal products derived from APEG-1 and the APEG-1 polypeptide can be used to diagnose and treat vascular conditions, e.g. restenosis, atherosclerosis, transplant arteriosclerosis or diabetes. at APEG-1 DNA, identified by differential expression in the aorta compared to ther organs, was used to obtain human APEG-1 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9700953-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Pages 37-38; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aortic preferentially-expressed gene APEG-1 - useful to develop prods, for diagnosis and treatment of vascular conditions, e.g. restenosis, atherosclerosis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hsieh C,
                                                                                                                                                                                                                                                                                                                                                             Sequence 1225 BP; 249 A; 363 C; 382 G; 231 T; 0 other;
                                      Human aortic-preferentially-expressed gene 1 cDNA
                                                                  05-JUN-2000
                                                                                            AAZ51043;
                                                                                                                      AAZ51043 standard; cDNA;
                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                            378
                                                                                                                                                                                         318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1997-087380/08
                                                                                                                                                                                                                                        CACCATACTCATTGACCGCTTTGCAAGTGTAGAAACCAGCATCGCCACGCTCTGCAGCCA 319
                                                                                                                                                                                                      aaatctgcagcgfagatatcacttcctctcccacctcc
                                                                                                                                                                                       GATCCGCAC CGCACAGCCCACCCTCAGCCTCCTCC
                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW10566
  aortic-preferentially-expressed gene-1; APEG-1;
striated muscle cell; vascular smooth muscle ce
                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee M;
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
78..419
/*tag= a
/label= APEG-1
                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0494577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US10636
                                                                                                                                                                                                                                                                                                            4.38;
                                                                     entry)
                                                                                                                           1228
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                               Score 38.8; DB Pred. No. 0.056;
                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                    Mismatches
        smooth muscle cell; VSMC;
                                                                                                                                                                                                                                                                                                                               DB 18;
                                                                                                                                                                                                                        689
                                                                                                                                                                                                .81
                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                             Length 1225;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                         Gaps
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antiarteriosclerotic; vasotropic; cis-acting transcriptional repressor; treatment; diagnosis; vascular disease; atherosclerosis; restenosis; chromosome 2q33-34; ss.
                                                                                                                                                Homo sapiens
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/*tag-
                       Location/Qualifiers 78..419
/*tag- a
/product- "APEG-1 protein"
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WO200009689-A2

14-AUG-1998; 30-APR-1999; 11-MAY-1999; 24-FEB-2000 98US-0134250 99US-0303069 99WO-US10298

(HARD ) HARVARD COLLEGE

Lee M, Hsieh C;

P-PSDB; AAY70077

2000-224334/19.

New gene useful for treating and diagnosing vascular diseases comprises a single gene encoding aortic-specific and striated-specific muscle cell isoforms

Disclosure; Fig 16; 88pp; English.

library. APIG-1 gene, located on human chromosome 293-34, encodes two muscle cell protein isoforms, one specific to aortic smooth encodes two muscle cell protein isoforms, one specific to aortic smooth muscle cells designated APEG-1 protein and the other specific to striated muscle cells designated SPEG protein.

APEG-1 protein can be administered to vascular smooth muscle cells (VSMC) to inhibit their prolliferation or migration at the site of vascular injury. The present sequence is used to screen vSMC-specific vascular injury. The present sequence is used to screen vSMC-specific expression. A enhancer sequence which is used to direct VSMC-specific expression of cis-acting transcriptional repressor sequence found in the 5' region of APEG-1 gene is useful to direct (compounds that bind to the repressor and increase APEG-1 expression in VSMC. APEG-1 is useful for treating and diagnosing vascular diseases such as alberosclerosis and restenosis. The present sequence is a cDNA encoding aortic-preferentially-expressed gene-1 (APEC-1) protein from a human lambda gtll aortic 5'-stretch cDNA

Sequence 1228 BP; 249 A; 363 C; 382 G; 231 T; 3 other;

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Query Match
Best Local
                      Matches
     61;
                            Similarity
                      Conservative
                           4.3%;
                        0;
                       Score 38.8; D
Pred. No. 0.05
0; Mismatches
                            NO. 0
                              0.056;
                                  DB
                                   21;
                         37;
                                   Length 1228;
                         Indels
                         0
                          Gaps
                           0
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В QΥ

В Ş

DEX PX XX RESULT 8
AAV48217/c
ID AAV48217 standard; DNA; 1238 AAV48217; ВP

Human aortic-preferentially-expressed gene-1

09-NOV-1998

(first entry)

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RESULT 9
AAV48218/c
ID AAV482
XX AAV482
AC AAV482
XX O9-NOV
DT 09-NOV
XX Uman
XX ds; h
KW smooth
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                                                                                                                                                                                                                                                                                                                                                              QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The aortic preferentially expressed protein 1 (APEG-1) can be used to derive an enhancer/promoter. This linked to a polypeptide coding sequence which regulates smooth muscle cell-specific expression of the polypeptide coding sequence can be used as a method of inhibiting vascular smooth coding sequence can be used as a method of inhibiting vascular smooth enuscle cell proliferation. The nucleic acids are used to direct developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental stage-specific expression of a heterologous polypeptide developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 16; 88pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1238
ds; human; striated muscle preferentially expressed protein; smooth muscle; cell proliferation; developmental stage; gamma-interferon; tissue plasminogen activator; p2l cell cycle; nitric oxide synthetase.
                                                                                 Human striated muscle preferentially expressed gene
                                                                                                                                                                                                                    AAV48218 standard;
                                                                                                                                  09-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                           328 GGATCCGCAGCCGGCACAGCCCACCCTCAGCCTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
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DB; AAW77047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human, rat or mouse aorta or striated-muscle preferentially ssed proteins - useful for treating e.g. atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ç,
                                                                                                                                                                                                                                                                                                                                                       aaatetgeagegtagatateaetteetteteeseacetee 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                     (first entry)
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/product=
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88..429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The striated muscle preferentially expressed protein (SPEG) can be linked to an enhancer/promoter derived from an aortic preferentially expressed gene to regulate smooth muscle cell-specific expression. This can be used as a method of inhibiting vascular smooth muscle cell proliferation. The nucleic acids are used to direct developmental stage-specific expression of a heterologous polypeptide which is stage-specific expression of a heterologous polypeptide which is especially selected from tissue plasminogen activator (LPA), p21 cell expression, nitric oxide synthetase, gamma-interferon, atrial cycle inhibitor, nitric oxide synthetase, gamma-interferon, atrial cycle inhibitor, nitric oxide synthetase, gamma-interferon strial cycle inhibitor. These are used to inhibit the proliferation of smooth muscle cells, e.g. for the treatment of atherosclerosis.
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useful for treating e.g. atherosclerosis % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{
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                                                                          Human; striated muscle preferentially expressed gene; SPEG; aortic-preferentially-expressed gene-1; APEG-1; striated muscle cell; aorta; smooth muscle cell; antiarteriosclerotic; vasotropic; treatment; diagnosis; vascular disease; atherosclerosis; restenosis;
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"No start codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a partial cDNA encoding human striated muscle preferentially expressed gene (SPEG) protein. This protein was detected in striated muscles of skeletal and cardiac tissues. Was detected in striated muscle cell protein isoforms encoded by It is one of the two muscle cell protein isoforms encoded by the aortic-preferentially-expressed gene-1 (APEG-1) located on human chromosome 2q33-34. The other protein isoform is specific to aortic smooth muscle cells designated APEG-1 protein. The present sequence can smooth muscle cells designated APEG-1 specific-promoter which may be be used to identify striated muscle cell specific-promoter which may be used to direct gene expression in striated muscle cells to treat diseases associated with these muscles. APEG-1 gene is useful for treating and diagnosing vascular diseases such as atherosciarosis and reconstructions.
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30-APR-1999;
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3..1988
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                                                                                                                                                                                                                                                                                                                                                                                                            963 C; 920 G; 411 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                          ВP
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                                                                           the entire Histidine-rich
                                                                                                                                                                                                                                                                                                                                                                       DB 21;
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RESULT 12 AAH25568/c

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ATCCTGATCATGATGCTGCTGCTGGTGCATCGTGATGATGATGGTGGTGGT 1278 atgcqqatqctqtagqtgqaqqaaggatqqatatcaatgatgqtgqccqaqtt 379

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Two variants of HiskP are produced by P. falciparum. One is associated with what is referred to as "knobby phenotype" (K30) and associated with what is referred to as "knobby phenotype" (K30) and associated with what is referred to as "knobby phenotype" (K30) and associated with what is characteristic of the vehicles of perfection. It has now been found that cDNA expressing arythrocyte infection. It has now been found that cDNA expressing cerythrocyte infection. It has now been found that cDNA expressing arythrocyte in the genomic clone (AAUL5512) is encoded in two expressing that the signal the continuing that synthesis of the protein occurs via the properties. Other, probes you have synthesis of the protein occurs via the properties. Other, probes synthesis of the protein occurs in a continuing that synthesis of the protein occurs via the properties. Other, probes synthesis of the protein sequences in a confine numerous tandem repeats with up to nine histidine residues in a cow, similar to other plasmodium proteins for which sequence data
                                                                   Query Match
Best Local
                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                   Histidine-rich protein associated with plasmodium knob phenotype and DNA encoding it, used for in vitro diagnosis of {\bf P}_{\rm c}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-199590/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SLOK ) SLOAN KETTERING
                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 7A-B; 20, 3; English.
                                                                                                                                                                                                                                                                                                                                                                                        Falciparum
                                                                                                                      Sequence 1648 BP;
                 267 Leegreegtgalgglgaletegtlgelgggeteaclettlgecaateeggttettggegtae 326
66;
                                                                    Similarity
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                                                         Conservative
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563..1477
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360..490
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                                                                       Score 37.8; DB 13; pred. No. 0.13;
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                                                            Mismatches
                                                                                                                               441 T; 0 other;
                                                              47;
                                                                                       Length 1648;
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CC designated Nov2. The protein is a membrane boun. Id secreted protein.

CC designated Nov2. The protein is a membrane boun. Id secreted protein.

CC nov polypeptides and polynucleotides are useful for treating or a preventing a Nov-associated disorder, and in the manufacture of a preventing a Nov-associated with a human disease such not consider the protein of the manufacture of a solv-associated disorder. They are also useful for treating disorders as Nov-associated those involved in development, differentiation as of constant on of the protein the pathologies related to and activation of the protein the pathologies of several human and activation of the protein the pathologies of several human accomplastas, in disease or pathologies of cells in blood circulation and constant of the pathologies of several disorders and/or pathologies, autoimmune and inflammatory diseases.

CC cardiovascular diseases, metabolic diseases, cancer growth and content of the pathologies of several activation activation activation of the pathologies.

CC cardiovascular diseases, metabolic diseases, cancer growth and content of the pathologies of several activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation a
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Matches 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  secreted protein; blood circulation;
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10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 15-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel
                                                                                                                                                                                         leukemia, in gliomas, neurological diseases, neurodegenerative disorders. Alzheimer's disease, Parkinson's disorder, and hematopoietic disorders. NOV polypeptides and polynucleotides are also useful for treating neurodegenerative disorders, immune disorders and hematopoietic
                                                                                                                     Sequence 1887
                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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ntion and treatment of a broad range of pathological
       81;
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99US-0170230
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                                                                                                                                259
                                 4.1%; 52.6%;
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          ; Score 37.2; D; Pred. No. 0.22 0; Mismatches
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                                                                                                                                     577 G;
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                                         DB
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RESULT 13
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XX 11-JAN
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 382.
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30-JUN-2000;
07-JUL-2000;
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24-FEB-2000;
02-MAR-2000;
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2000US-0198123.
2000US-0205515.
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2000US - 0224518

2000US - 0224519

2000US - 0225213

2000US - 0225264

2000US - 0225266

2000US - 0225267

2000US - 0225267

2000US - 0225270

2000US - 0225270

2000US - 02254757

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2000US - 0226681
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2000US-0216880
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CC specification. The nucleic acids, proteins, antibodies and (ant)agonists (c) are useful in the discussis, trealment and prevention of: (a) cancer, (c) are breast and overiar cancer and other cancers of the adrenal gland, (c) bone, bone marrow, breast, dastrointestinal tract, liver, lung, or (c) troughtial; (b) immune discusders e.g. Addison's disease, allergies, (c) autoimmune based prices and autointee based in the gradies and contributes (d) disbetes mellitus, (c) cardiovascular disorders such as myocardial ischaemias; (c) colitis; (c) cardiovascular disorders such as myocardial ischaemias; (c) wound healing; (e) neurological diseases e.g. cerebral anoxia and (c) printed specifications diseases such as viral, bacterial, fungal (c) and parasitic infections.

CC and parasitic infections.

CC printed specification, but was obtained in electronic format directly from wipo at tip-wipo-int/pub/published_pot_sequencees.
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Matches 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acids treating and/or preventing
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                                         3700 GCGGGGGGUTCACAGCTGGTGGTTGGCTAGCTGAGGAGGTGGTGGGGGGACCCAGAGTCA 3641
                                                                                                                                                                     Sequence 8269
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gttyaallatteeaeggteeteeeegtatgaattgatageatggeaggaggaagaaaeegg 630
                                                          gcyagcılıqacalctcılqalctcaatctcygygagyatctgygygyttcttycactytya 570
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                                                                                                   Score 37.2; D
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2000US-0246511.
2000US-0246611.
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RESULT 14
AAX98114/C
ID AAX981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of ORF21421 encoding a virulence factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX98114;
                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a Pseudomonas aeruginosa nucleic aidd sequence. P. aeruginosa is an opportunistic human pathogen present in sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a parametric air activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUN-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 4; 228pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virulence factors useful in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ausubel F,
                                                                                                                                                                                                                                                                                                       is a P. aeruginosa infection.

note: the sequences given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely it is therefore possible that the sequence given below is not entirely.
                                                                                                                                                                                                                                                            Sequence 1341
                                                                                          437
                                                                                                                          371
 251
                               497
                                                                                                                                                                                  Local Similarity
les 97; Conserv
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                                                                                                                        GCTCGCCTGGGGGAATGACGGTGGTCTTTCTGAACGGGTTGACTTGGGAGTGCGTCACC
                                                                                                                                     gttcagctgaggggaaacatctttggttctctgagcagaatcccacgagtctgatttatt 436
                                                           AACTCATGCTCGATGGCATAGCCCCAGATCGTCCGCAGATvATTCGAGTACGTGTTCCAG
                                                                               tttgcattcacactgtcalagcctgtgatgyggctgttgccatcaaaccccatggtccac 496
CTCCGCTTGGACAGGCCTTGTTCCAGTACCTTGCGTCGCCATCCCAGGACAGCCCGGTGG
                   ctgagcgtgatggtgcgagctttgacalctctlgatctcaalctcggggaggatclggggg
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                                                                                                                                                                                    4.18;
nilarity 49.28;
Conservative (
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                                                                                                                                                                                                                                                                   A; 430 C;
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                                                                                                                                                                                                                                                                      380 G;
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AAX98035/c
ID AAX98035 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX98035;
                                                                                                                                                                                                                                                                                                                                The present sequence represents a Pseudomonas aeruginosa nucleic aicd sequence. P. deruginosa is an opportunistic human pathogen present in sequence. P. deruginosa is an opportunistic human pathogen present in sequence of water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a parameters insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human pathogen; virulence polypeptide; virulence
pathogenic infection; Pseudomonas aeruginosa infe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09927129-A1
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                                                                                                            21791 GCTCGCCTGGGGGAATGACGGTGGTCTTTCTGAACGGGTTGACTTGGGAGTGCGTCACC 21732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 TCCACGTCCTGTACGGT
                                                                                                                                                                                                                                                                                                                        is a P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 228pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virulence factors useful in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-357851/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ausubel F,
 21671
                                                                                                                                                                                                                                                                              is a P. aeruginosa injection.

note: the sequences given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely
                                                                                                                                                                                                                                        Sequence 42235 BP;
                            497
                                                                                    437
                                                                                                                             gttcagcigaggggaaacatctttggttctctgaggagaatcccacgagtctgatttatt 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , 9J
CTCCGCTTGGACAGGCCTTGTTCCAGTACCTTGCGTCGCCATCCCAGGACAGCCCGGTGG
                                                      AACTCATGCTCGATGGCATAGCCCCCAGATCGTCCGCAGATGATTCGAGTACGTGTTCCAG
                                                                        tttgcattcacactgtcatagcctgtgatggggctgttgccatcaaaccccatggtccac 496
               ctgagcglyatggtgcgagctttgacatctctttgatctcaatctcgggaggatctggggg 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cao II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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  1 US-08-494-577-11
2 US-08-795-868-11
3 US-08-795-868-13
1 US-08-232-463-14
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1 US-08-494-577-2
1 US-08-68-395A-2
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Qy 592 ccccytatyaattqatagcatggcaggagaagaaaccggaatcttctctccactgttggca so	Query Match 4.3%; Score 38.8; DB 1; Length 122 Best Local Similarity 62.2%; Pred. No. 0.0056; Matches 61; Conservative 0; Mismatches 37; Indels	RESULT 1 US-08-494-577-11/c US-08-494-577-11/c Sequence 11, Application US/08494577 PATCENT NO. 5786171 GENERAL INFORMATION: APPLICANT: Lee, MI-En APPLICANT: HS; bi, Chunq-Minq TITLE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: FISH & Richardson P.C. STREET: 225 Franklin Street CITY: BOSTON STATE: MA COUNTRY: USA ZIP: 02110-2804 COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER: ISM PC COMPAINED COMPUTER: 15M PC COMPAINED COMPUTER: 15M PC COMPAINED COMPUTER: 15M PC COMPAINED COMPUTER: 15M PC COMPAINED COMPUTER: 15M PC COMPAINED COMPUTER: 15M PC COMPAINED COMPUTER: 15M PC COMPAINED CONFORMATION NUMBER: 446 ATTORNEY/ACENT INFORMATION: TELLENCOMMUNICATION INFORMATION: TELECOMMUNICATION INFO	ALIGNMENTS	29.6 3.3 2571 4 US-09-234-393-12 29.6 3.3 2774 4 US-09-363-189B-5 29.6 3.3 4285 4 US-09-040-774-1 29.6 3.3 4285 4 US-09-040-774-1 29.4 3.3 890 4 US-09-475-316A-34 29.4 3.3 913 4 US-09-475-316A-32	36 29.6 3.3 1013 4 US-09-475-316A-30 37 29.6 3.3 2424 4 US-09-234-393-1 38 29.6 3.3 2525 4 US-09-234-393-39 39 29.6 3.3 2528 4 US-09-234-393-37 39 29.6 3.3 2528 4 US-09-234-393-41	C 29 29.8 3.3 1335 3 US-09-167-354-6 Sequen C 30 29.8 3.3 2614 2 US-08-985-090-1 Sequen C 31 29.8 3.3 2689 2 US-08-985-090-1 Sequen C 32 29.8 3.3 2689 3 US-09-167-354-5 Sequen C 33 29.8 3.3 2699 3 US-09-167-354-5 Sequen C 34 29.6 3.3 269 3 US-09-476-124-43 Sequen C 35 29.6 3.3 208 4 US-09-476-124-43 Sequen C 35 29.6 3.3 208 4 US-09-476-124-43 Sequen	28 29.8 3.3 1335 3 US-09-165-543-3 S
ctractgttggca 651	th 1225; els 0; Gaps	ENE AND		Sequence 12, Appl Sequence 5, Appli Sequence 1, Appli Sequence 34, Appl Sequence 32, Appl	1, App1 1, App1 39, App 37, App 41, App	15, Appl 15, Appl 1, Appl 1, Appl 5, Appl 11, Appl 11, Appl 43, App	, ,,

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                                                Sequence 13, Application US/08795868
Patent No. 5846773
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Rest Local Similarity 62.2%;

Matches 61; Conservative
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PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/494,577
APPLICATION UMBER: 08/494,577
FILING DATE: 22-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 11:
                                      GENERAL INFORMATION:
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APPLICANT: Hsieh, Chung-Ming
TITLE OF INVENTION: A SINGLE GENE ENCODING AORTIC-SPECIFIC
TITLE OF INVENTION: AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & Richardson, P.C
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TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
APPLICANT: Lee, Mu-En
APPLICANT: Hsieh, Chung-Ming
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; LOCATION: 3...198; OTHER INFORMATION: US-08-795-868-13
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SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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FILING DATE: 06-FEB-15
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05
                                                                                                                                                                               GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,819
REFERENCE/POCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA
                                                                                  APPLICANT: DÖRNER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FAIKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    1887 GGATCCGCAGCCGCGCACACCCTCAGCCTCAGCCTCCTCC
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SOFTWARE: FastSEC
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REGISTRATION NUMBER:
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                                                                       Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A SINGLE GENE ENCOUING AORTIC-SPECIFIC AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
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                                                                                Sequence 2, Application US/08494577 Patent No. 5786171 GENERAL INFORMATION:
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MEDJUM TYPE: Floppy
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REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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NAME: BENT, Stephen A.
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LENGTH: 7218 base pairs
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         APPLICANT: Lee, Mu-En
APPLICANT: Heieh, Chung-Ming
TITLE OF INVENTION: AORTIC PREFERENTIALLY EXPRESSED GENE AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 12
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CORRESPONDENCE ADDRESS
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MOLECULE TYPE: DNA
US-08-494-577-2
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MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 617/542-5970
TELEFAX: 617/542-8906
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CITY: Boston
STATE: MA
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APPLICANT: HSTeb, Chang-Ming
APPLICANT: HSTeb, Chang-Ming
APPLICANT: HSTeb, Chang-Ming
TITLE OF INVENTION: A SINGLE GENE ENCODING AORTIC-SPECIFIC
TITLE OF INVENTION: AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
             SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795,868 FILING DATE: 06-FEB-1997 CLASSIFICATION: 424
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STREET: 225 Franklin Street
                                                                                                                                   ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: single
PRIOR APPLICATION DATA:
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                                                                                               COMPUTER: IBM CON
OPERATING SYSTEM:
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                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street
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pred. No. 0.019;
0; Mismatches 38;
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APPLICATION NUMBER: 08/49
FILING DATE: 22-JUN-1995
ATTORNEY/AGENT INFORMATION:

08/494,577

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                                             TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTEKISTICS:
LENGTH: 1308 base pairs
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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st Local Similarity 60.8%;
.atches 59; Conservative
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APPLICANT: Hsieh, Chung-Ming
TITLE OF INVENTION: AORTIC PREFERENTIALLY EXPRESSED GENE AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                          APPLICATION NUMBER: US/OF FILING DATE: 22-JUN-1995 CLASSIFICATION: 436 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Florpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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MEDIUM TYPE: Florpy
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REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
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MOLECULE TYPE:
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                 STRANDEDNESS: single
TOPOLOGY: linear
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US-08-494-577-1
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Best Local Similarity
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                                                                                                                             Query Match 4.0%;
Best Local Similarity 60.8%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Listeh, Chung-Ning
TITLE OF INVERTION: A SINGLE GENE ENCODING AORTIC-SPECIFIC
TITLE OF INVERTION: AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/494,577
FILING DATH: 22-JUN 1995
APTORNEY JAGENT INFORMATION:
NAME: FIGSEL, Jamis K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM.
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: 05/08/795,868
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                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                             470 CGCCATATTCGTTGACCGCCTTGCAAGTGTAGAAACCAGCATCTCCCCTCTCAGCAGCCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: 1908
SOFTWARE: PastSEQ for Windows Version 2
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ZIP: 02110-2804
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410 GGATCCTCAACCGGCAGAGCCCACCCTCGGCCTCCTC 374
                             652 aaatetgeagegtagalateactteeteteecacete 688
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fraser, Janis K
REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                             STRANDEDNESS: double
                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                INFORMATION:
                                                                                                                                                                                                                                                                             nucleic acid
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                                                                                                                                                                                                                                                                                              1308 base pairs
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                                                                                                                                    0; Mismatches
                                                                                                                                                  Score 36.2; DB Pred. No. 0.043;
                                                                                                                                                                    DB 2;
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                                                                                                                                                                      Length 1308;
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                                                                                                                                        Gaps
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∪S-08-068-395A-2/c
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Patent No. 5496719
US-08-068-395A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/068,395
FILING DATE: 1930527
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-135254
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
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APPLICANT:
APPLICANT:
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APPLICANT: ASAMI, OSAMU
APPLICANT: SUGIYAMA, HIDEHIKO
DEKOBA, CHIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LDEKOBA, APPLICANT: HOSHINO,
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 5-44014
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5496719man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 5-44013
FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 68
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                    LENGTH: 1755 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                  LOCATION:
                                                                                                                                                                                       ORGANISM:
                                                                          LOCATION:
                                   NAME/KEY:
                                                                                            NAME/KEY:
                     LOCATION
                                                                                                                                                 NAME/KEY:
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KAJINO, TSUTOMU
IMAEDA, TAKAO
SAKAI, KIYOKO
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1755 S. Jefferson Davis Highway, Suite 400
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110..1624
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                   mat_peptide
170..1624
                                                                          sig_peptide
110..169
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                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                            cDNA to mRNA
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Best Local Similarity 56.1%;
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APPLICANT: YAMADA
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                                                             TELEFAX: (703) 413-2221
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PRODUCING THE SAME
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MEDIUM TYPE: Floppy disk
COMPUTER: HM PC comparible
COMPUTER: HM PC comparible
COMPUTER: HM PC comparible
NO OPERATING SYSTEM: M DOS/MS:103
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                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 GURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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NAME: Oblon, No. 5700659man
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 04-MAR-PRIOR APPLICATION DATA:
                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1755 S. CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: HS/08/464,365
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                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 04-MAI
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                                                                                                          TELEPHONE: (703)
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                                             ENCTH:
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Y: U.S.A.
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                            nucleic acid
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IMAEDA, TAKAO
SARAI, KIYOKO
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1755 S. Jefferson Davis Highway, Suite 400
                                              1755 base pairs
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HOSHINO, FUMIHIKO
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linear
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                  double
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US-08-464-365-2
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                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1)..(1554)
US-09-043-123-1
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Patent No. 609652
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 1
LENGTH: 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HAAS, Rainer
APPLICANT: ODENBREIT, Stefan
APPLICANT: MEYER, Thomas F.
APPLICANT: BLUM, Andre
APPLICANT: BLUM, Andre
APPLICANT: CORTHESY-THEULAZ, Irene
APPLICANT: CORTHESY-THEULAZ, Irene
TITLE OF INVENTION: NEW ADHESIN FROM HELICOBACTER PYLORI
FILE REFERENCE: 05648004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: C
ORIGINAL SOURCE:
ORGANISM: Humi
                                                                                                                                                                                 Query Match
Best Local Simila ity
Matches 77; conserv
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                                                                                                                                                                                                                                                                                                                          ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                              FEATURE:
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    .1246
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                                                                                                                      1126 tacygottolicagotalaacygogogggcylyggtaalggcoctacttacaatcaagic 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                         668 tatcacttcctctcccacctccttggtggatacagtacgggccactttcaggggttaatga 727
                                                                         728 teciqtetetetetecageggacaatgatgggeteteccatgggetgtgcageteatte 787
ggtagtaggaglcttaatgcgggcttctttggg 1278
                   cttcctttgaccctgatggccaggtggtgtggg 820
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110..1624
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110..169
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170..1624
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                                                                                                                                                                                                        3.5%;
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                                                                                                                                                                                             0
                                                                                                                                                                                                        Score 31.4; DB 3; Length 1557; Pred. No. 1.9;
                                                                                                                                                                                              Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1755;
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US-08-324-243-34/c
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APPLICALLY
FILING DATE: 19-SEP-1974
FILING DATE: 19-SEP-1974
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T
REGISTRATION NUMBER: 30.162
REFERENCE/DOCKET NUMBER: 00786
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5970
TELEPHONE: (617) 542-5970
TELEFAX: (617) 542-8906
TELEFAX: 2.0154
INFORMATION F.M. SEO ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1632 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/08324243
Patent No. 5786464
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                       RESULT 13
US-08-532-390-34/c
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                                                                                                                                                                                                                                                                                Sequence 34, Application US/08532390 Patent No. 5795737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: OVEREXPR
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-1005/MS-1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 225 Franklin
CITY: Boston
STATE: Massachusetts
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTEK: IBM PC compatible
                                                                                                                                                                                    TITLE OF INVENTION: High Level Expression of Proteins NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                         APPLICANT: SEED, BRIAN APPLICANT: HAAS, JURGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/324,243 FILING DATE: 19-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                               495 GTTGGTGGTGCTCCCCCAGGTCGGTGCAGTTCAGGGTCACGCACAGGGGGGGTCAGCTTCA 437
                                                                                                                                                                                                                                                                                                                                                                                                                       323 gtacalurygalurclylagulygagulagagulygatatcaatgatggtggccgagttca 381
                                                                 STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                            CITY: Boston
STATE: Massa
                                                   ZIP: 02110-2804
                                                                                                                               STREET:
                                                                                                                                                 ADDRESSEE:
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225 Franklin Street
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                                                                                                                                   225 Franklin Street
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                                                                                                                                                   Fish & Richardson P.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00786/226001
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US-08-717-294-34/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6114148
GENERAL INFORMATION:
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SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 00
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5970
TELEPAX: (617) 542-8906
TELEX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,243
FILING DATE: 19-SEP-1994
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LENGTH: 1632 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                 21P: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SEED, BRIAN APPLICANT: HAAS, JURGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 otcalocgccgtgatggtgatctcgttgctgggctcactcttgccaatccggttcttggc 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 gtacaıgoggatgotgtaggtggaggaagggtggatatcaatgatggtggccgagttca 381
                                                                                                                                                                                                      SOFTWARE: FASTSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: LECH, KAREN F.
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                   APPLICATION NUMBER: US/O:
APPLICATION NUMBER: US/O:
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            STREET: 176
CITY: Boston
                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                      FILING DATE
                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                              02110
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                                                                                                                                                                                                                                                         1BM Compatible
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                                                                                                                                                                                                                                                                             Diskette
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53.8%;
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                                            00786/345001
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; TOPOLOGY: II; MOLECULE TYPE: US-08-717-294-34
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PCT-US95-11511-34/c
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                                                                                                                                  ; TOPOLOGY: linear PCT-US95-11511-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application PC/TUS9511511 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                            Matches
                                                                          Query Match
Best Local :
                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SEED, FRIAN
TITLE OF INVENTION: OVERHEXPRESSION OF MAMMALIAN AND VIRAL
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALIABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1HM PC compatible

COMPUTER: 1HM PC compatible

COMPARTIC SYSTEM: PC 1035/MS:1035

SOFTWARE: Fatentin Pcfcase #1.0, Version #1.30B

CURRENT APPLICATION NUMBER: PC1/US95/11511

APPLICATION NUMBER: PC1/US95/11511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 clcatecqccqlqatgglgalclcgtlyctgygctcactcttgccaatccggttcttgqc 322
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 gtacaturuqatyclqlaqq1qqaggaaggqtqakatcaatgatggtggccgagttca 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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263 ctcatccqccgtqatgqtga(ctcgttgctgggctcactcttgccaatccggttcttggc 322
                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
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                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
                                                                            similarity
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                                                                                                                                                                                                1632 base pairs
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                                                            3.5%;
ailarity 53.8%;
Conservative
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pred. No. 2.7;
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                                                                          Score 31; DB 5; Length 1632; pred. NO. 2.7;
                                                                 0;
                                                                  Mismatches
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                                                                      55;
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Scarch completed: March 4, 2002, 05:12:49

Job time: 17023 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l number of hits satisfying chosen parameters:
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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501
1 gcttttcgccagcatcaata.....aacacacggacttcagatac 501
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## SUMMARIES

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11	10	13	13	13	13	11	11	13	11	10	11	BG
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## ALIGNMENTS

,	FEATURES					COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORLDS	VERSION	ACCESSION	001111100	LOCUS	BF348620	RESULT 1
	Location/Qualifiers	http://image.lln1.gov Plate: LLAM9426 row: p column: 05 High quality sequence stop: 697.	DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	<pre>cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)</pre>	Tissue Procurement: David N. Louis, M.D.	Contact: Robert Strausberg, Ph.D.	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.		Eukaryota; Metazoa; Chordata; Craniata; Vertebraca; Eucereoscomi; Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.		human.	EST.	BP348620.1 GT:11296215	BF348620		602019924F1 NOT COAP Brn67 Homo sabiens cDNA clone IMAGE:4155508		

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Contact: Smith
                               Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                              Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett Gasas, E., Watton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pericea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                            Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; I (bases i to 712)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections.
                                                                                                                                                                                                                                                                                                            HF528580 712 lp mRNA
602043580F1 NC1_CGAP_Brn67 HC
5', mRNA sequence.
BF528580
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PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 98 row: A column: 1
Seq primer: ATTTAGGTGACACTATAG.
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Contact: Robert Strausberg, Ph
                          Unpublished (1999)
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/tissue_type-"pooled"
/lab_host-"DH10B"
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/db_xref="taxon:9913"
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Pred. No. 1.4e-62;
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                                                                                                                  AACAATAGAAGCTTTGACAC
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Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Plate: LLAM9493 row: p column:
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CNS02UJS 1008 bp DNA GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
167120 of library G from Tetraodon nigroviridis, genomic survey
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note-"Organ: brain; Vector: pCMV-SPORTB; Site_1: Note site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 210 c 204 g 118 t
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/clone_lib-"NCI_CGAP_Brn67"
/Lissue_type="anaplastic oligodendroglioma with
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/db_xref="taxon:9606"
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Pred. No. 1.6e-28;
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                                                                                        Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases | to 1008)
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AL214561
AL214561.1 G1:7873380
GSS; genome survey sequence.
Tetraodon nigroviridis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, E., Sanrin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
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2 (bases 1
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Bouncau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
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/db_xret."Laxom:99883"
/clone="...7120"
/clone-"...7120"
/clone-"...7C0"
/clone-"...7C0"
/clone-"...7C0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUC-OLI"
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310 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86.4; DB 13;
Prod. No. 1.4e-13;
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   15-MAR-1995
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DEFINITION

HSC2XA021

normalized

infant brain cDNA Homo sapiens cDNA clone

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COMMENT
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ry Match
st Local Similarity
atches 101; Conserv
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F13426
F13426.1 G1:710043
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IMAGE: molecular integration of the analysis of the human genome
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1,rue de l'Internationale, BP60 91002 i/RY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genexpress_library_idt: C: Genexpress_sequence_idt: y2c-2xa02
Seq primer: (-21)M13_universal.
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                         Z45894 294 bp mkNA EST 14-NOV-1994
HSCZWH041 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                         EST.
                                                                                                                                                                                                    Z45894
                                                                                                                                                                                                                              c-zwh04, mRNA sequence.
                                                                                                                                                                245894.1 G1:575128
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/dev_stage="3 months old"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/note="forgan: brain; Vector: lafmid BA; Site_1: HindIII;
/note="forgan: brain; Vector: lafmid BA; Site_1: HindIII;
/stolate=muscular atrophy patient; tissue_type=total brain
/stolate=muscular atrophy patient; tissue_type=total brain
/stolate=muscular atrophy patient; tissue_type=total brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-2xa02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="normalized infant brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.5%;
87.1%;
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Pred. No. 9.3e-13;
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                          Craniata; Vertebrata; Enteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
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Cedex, FRANCE
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MEDLINE
COMMENT
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SOURCE
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FR0022054
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                                                                                     REFERENCE
AUTHORS
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Best Local
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                                                                                                                                                                                        ORGANISM
                                                     TITLE
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                                                                                                                                                                                                                                                                                                                                                                                 AGTTTAGCTGAAATGCTCATGAGTAAGANTACCCGGGACTTCAGNTAC 107
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C. R. Acad
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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
Sebastiani-Kabaktchis,C. and Tessier,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
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Seq primer: (-21)M13_universal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genexpress-Genethon
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AcanthOmorphic, .....
Tetraudontidae; Takifugu.

1 (bases 1 to 612)
1 (bases 1 to 612)
2 (clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Elqar,G., Clark,M., Smith,S.,
Williams,G. and Brenner,S.
Direct Submission
Submitted (O8-DEC-1997) MRC Human Genome Mapping Project Resource
Submitted (O8-DEC-1997) MRC Human Genome Mapping Project Resource
Submitted (O8-DEC-1997) MRC Human Genome Mapping Project Resource
                                                                                                                                                                                          Takifugu rubripes.
Takifugu rubripes
                                                                                                                                                                                                                                                             F.rubripes GSS sequence, clone 070M05aA12, AL014925
                                                                                                                                     Eukaryota: Metazoa; Chordala; Craniata; Vertebrata; Euteleostomi; Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoreleostei Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiiormes;
                                                                                                                                                                                                                                              AL014925.1 G1:2681293
                                                                                                                                                                                                                             GSS; genome survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib-"normalized infant brain cDNA"
/sex-"Female"
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/clone-"c-zwh04"
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/dev_stage-"3 months old"
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89.7%;
                                                                                                                                                                                                                                                                                                    612 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 80.2; DB 1
Pred. No. 4.9e-12
0; Mismatches 1
                                                                                                                                                                                                                                                                                                      DNA
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91002 EVRY
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Cedex, FRANCE
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PRIMER:
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Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource
Submitted (19-JUN-1998) MRC Human Genome Mapping Project Resource
Control Hinxton, Cambridge, CB10 1SB, UK. Email:
                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 619)
Elgar, G., Clark, M., Smith, S., Meek, S.,
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.
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                                                                                                                                                                                                                                                 V_type: phagemid
PRIMER: KS
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Vector: pBluescript II KS
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/db_xref="taxon:31033"
/clone_lib="cosmid 070M05"
/clone="070M05aA12"
/clone="070M05aA12"
                                                                                       /organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone=lib="cosmid 096F20"
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153 c 154 g 168 t
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                Score 46.4; DB 13; Pred. No. 0.018;
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Best Local Similarity 53.5%;
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1 (bases | to 601)

Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Breuner,S.
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Takifugu rubripes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk Vector: pHluescript II KS
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AL027122.1 GI:3264465
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                  Takifugu rubripes
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/db_xref-"taxon:31033"
/clone_lib-"cosmid 070M05"
/clone-"070M05aB4"
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                                                                                                                                                                          Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda,
Fax: (301) 496 5239
                                                                                                                                                                                                                                                                                                               Genome R
20568492
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Submitted (09-JUN-1998) MRC Human Genome Mapping
Centre, Hinxton, Cambridge, CB10 ISB, UK. Email:
biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMEP: KS
                                  http://www.niddk.nih.gov/intram/people/boliver.htm Tissue isolation and library construction performed at the National Institute of Diabetes and Digestive and Kidney Diseases, NIH (see http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov).
                                                                                                                                                                                                                                                                                                                                                      Gene discovery using computational and microarray analysis transcription in the drosophila melanogaster testis
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 412)
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1 (bases 1 to 614)

1 (bases, Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y.,
                                                                                                                                                                                                                                                                                         On Aug 17, 1999 this sequence version replaced gi:5735990
                                                                                                                                                                                                                                                                                                                                                                                                                   Andrews, J., Bouffard, G.G., Cheadle, C., Lu, J., Becker, K.G. and
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/clone="096F20cC11"
144 c 154 g 141
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/db_xref="taxon:31033"
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Pred. No. 1.1;
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RESULT 12
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Best Local Similarity
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                                                                                    http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 47 row: f column: 09
                                                                                                                                                                                                                                                             Laboratory of Cellular and Developmental Biology NIDDK, National Institutes of Health 6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, Fax: (301) 496 5239 Email: oliver@helix.nih.gov,
                    Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1. .617
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Contact: Brian Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                      Andrews, J., Bouffard, G. and Oliver, B. Drosophila melanogaster testis expressed
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/strain="y[*] w[67c1]/Y"
/db_xref="taxon:7227"
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/lab_host="SOLR (Stratagene)"
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Pred. No. 1.1;
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RESULT 13
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TITLE
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                                                                                                                                                                                                                                                                                                                                 Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, km Bl-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: oliver@hellx.nih.gov,
                                                                                                                                                                                                        http://www.niddk.nih.gov/intram/people/boliver.htm Tissue isolation and library construction performed at the National Institute of Diabetes and Digestive and Kidney Diseases, NIH (see http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing and analyses performed by National Institutes of Health Intramural
                                                                                                                                                         Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 61 row: d column: 09
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Drosophila melanogaster testis expressed sequence tags
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melanogaster cDNA clone bs61d09 5', mRNA sequence.
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                                                                                                     primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/note="Organ: testis; Vector: pBlueScript SK (Stratagene);
Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
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/organism-"Drosophila melanogaster"
/strain="y[*] w[67c]]/Y"
/db_xref-"taxon:7227"
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/db_xref="taxon:7227"
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Celniker, S. and Rubin, G.M.

HIGP/HHMI AT Drosophila EST Project
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Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11569613.
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit qenomic AE003460: arm:2R [18105561,18403467]
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Site_1: EroR I; Site_2: Xho I; Testes dissected from 1-day adult y(*) w(67cl)/Y males raised at 25oC. RNA isolated using Trizol (Life Technologies) and a single
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library constructed using Stratagene ZAP-CDNA syntesis
kit. Oligo dT-primed, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
/clone="AT20576"
/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
                                                                                    /organism-"Drosophila melanogaster"
/db_xref-"taxon:7227"
                                                                                                                                                                                                                                  Location/Qualifiers
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/lab_host-"SOLR (Stratagene)"
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Matches 62; Conserv
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC: see http://www.nisc.nih.gov).
Plate: 54 row: i column: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, km Bl-13, Helhesda, MD 20892 USA
Fax: (301) 496 5239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Brian Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 646)
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Drosophila melanogaster testis expressed sequence tags
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primer: M13RP1 reverse primer (AB1).
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/dev_stage="0-3 day old ore-R males"
/dev_stage="0-3 day old ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha TonA"
/note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoR1;
/note="organ: ADULT testes; Vector: pOTB7; Site_1: EcoR1;
Site_2: Xhol; The mRNA for the testis library was made;
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
a 202 c 167 g 105 t
/note-*Organ: testis; Vector: pBlueScript SK (Stratagene); Site_1: EcoR I; Site_2: Xho '; Testes lissected from 1-5 day adult y[*] wf67c1]/Y males raised at 25oC. RNA isolated using Trizol (Lite Technologies) and a single round of Poly(A): selection using Oligotex (Qiagen). cDNA
                                                                                                                                                                                                                                    /organism="prosophila melanogaster"
/strain="y|*| w[67c1|/Y"
/db_xref="taxon:7227"
/cione="bs54f11"
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                  /dev_stage="1-5 day adult"
/lab_host="SOLK (Stratagene)"
                                                                                                                                                                                                            /clone_lib-"Drosophila melanogaster adult testis library"
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library constructed using Stratagene ZAP-cDNA syntesis kit. Oligo dr-primed, size fractionated ~1-6 kb, and directionally cloned at EcoRI and XhOI in Uni-ZAP XR. Following a single round of amplification pBlueScript SK phagemids were mass excised. A distribution channel for clones is being sought, but not currently available. Requests for clones cannot be honored.
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Query Match Best Local Similarity Matches 441 TGGTGTCCCTGGCTGGTGGTGATAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGTGC 382 345 teginaceatelectgeatectgqteggggttetaetgetetttgtgettetgetggttg 404 62; Conservative 7.9%; u; Mismatches Score 39.8; DB 11; Pred. No. 1.3; 37; ludels Length 646; 0; Gaps

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TGCTGGTGGTACTGCGGGGTGGTGACTCTGCATAGGCTGA 343

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Copyright (c) 1993 - 2000 Compuşen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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New isolated Down's Syndrome-cell adhesion molecule -develop products for detection, diagnosis and therapy developmental and neurological abnormalities

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ps-CAM; hown syndrome cell adhesion molecule; neural cell; signal transduction; trisomy 21; mental relardation; holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; mouse; ds; ss.
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                                 'AAV31981;
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Pred. No. 5.1e-148;
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This cDNA clone codes for hown syndrome-cell adhesion molecule CC DS-CAMI (see AAW42086), a cell surface glycoprotein belonging to a CC novel subclass of the lq superfamily with highest homology to CC neural cell adhesion molecules. A modified direct coMA selection CC between ETS2 and MXI by using cDNA from trisomy 21 human foetal CC brain. A unique cDNA iradment, designated E51 (see AAV31982), was CC obtained and used to screen a trisomy 21 human foetal brain (14 wk CC gestation) cDNA limitary. Finither clones were obtained by exon CC trappling clones. A splice variant clone was deduced from connembrane bound DS-CAM2007), was also identified. The CC non-membrane bound DS-CAM2007), was also identified. The CC 19422-223. The invention also provides murine DS-CAM partial consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host cells, consequences (see AAV31985-87), expression vectors and host 
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Query Match Best Local Similarity Matches 445; Conserv

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Best Local Similarity
Matches 350; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and MXI. E51 was used as a probe to screen the trisomy 21 foetal brain library. 62 Clones were isolated from the 2 million clones of the original library. overlapping clones were obtained that were used to deduce a full-length sequence (see AAV31981) coding for novel hown syndrome-coll adhesion molecule DS-CAM1 (see AAW42086). A splice variant, DS-CAM2 (see AAV31988), was also identified. DS-CAM polypeptides are associated with developmental and neurological processes. The polypeptides and nucleic acids are used to develop products for the detection, diagnosis and therapy of developmental and neurological and neurological seconds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 388 BP; 83 A; 119 C;
                                                                                signal transduction; trisomy 21; me holoprosencephaly; corpus callosum schizencephaly; diagnosis; assay; l
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                                                                                                                      DS-CAM2;
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                                                                                                                                                                                                                                                                                                                           GATGCTGGTGACCATCTCCTGTATCCTGGTGGGGGGTCTTGCTGCTGTTTGTGCTGCTCCTGCT
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                                                                                                                      bown syndrome-cell adhesion molecule; neural cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neural cell adh-sion molecules. A modified direct cDMA selection technique was applied to bacterial and Plantificial chromosomes between ETS2 and MX1 by using cDNA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk gestation) cDNA library. Further clones were obtained by exon trapping, and the complete DS-CAM2 cDNA sequence was identified trapping is a splice variant of membrane-bound DS-CAM1 (see AAW42086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Down's Syndrome-cell adhesion molecule -develop products for detection, diagnosis and therapy developmental and neurological abnormalities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA clone codes for Down synutures can account more on the DS-CAM2 (see AaW42087), an extracellular, soluble protein belonging to a novel subclass of the Ig superfamily with highest homology to a novel subclass of the American American American Street cDMA selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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aagayyetyeuayatyeaaagaytttagetyaaatuete 5175
                                                                       cctggtatgauntgcagatgcgggtgtgcaacagtgcgqgctgcqcggaqaagcagynta
                                                                                          cytuatatqaactqcagatgagagtgtgcaacaqcyccagctgtqcqgataagcaaqcca
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibiting translation of mkNA.
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AAI58196
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drayer Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                             Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polynucleotide SEQ ID NO
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                                                              Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activiny, inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                               The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM8642-AAM82213) with nootcopic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2000; 2000WU-US34263.
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                                                                                                                                                                                                                                                                Claim 1; SEQ 10 No 399; 10078pp; English.
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                                                                                                                                                                                                                                                                                             such as central nervous
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                           specification.
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                                       disorders.
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                Goodrich R,
                                                                                                                                                                                                                                                                                           polypeptides, useful for treating system injuries \dot{\cdot}
                                        tor this patent did
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Mismalches

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Score 140.8; DB 22; Prod. No. 4.4e-34;

Sequence

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other

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PR 23 - UIL 1999; 99US-0145276.

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PR 21 - AUG-1999; 99US-014708.

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PR 21 - AUG-1999; 99US-014708.

PR 21 - AUG-1999; 99US-014708.

PR 21 - AUG-1999; 99US-014708.

PR 21 - AUG-1999; 99US-014708.

PR 21 - AUG-1999; 99
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                               autoimmunohepatitis type II;
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                                                                                                                                                                                                                                                                                                                                                               Human; cytochrome P450IId6; liver/kidney microsome; tKM-1; antibody; autoimmunohepatitis type II; AIH type II; hepatitis C virus; ss.
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                                                                                      WPI; 1998-292131/26.
P-PSDB; AAW44870.
                                                                                                                                                                            24-SEP-1996;
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                                                                                                                          (HOKE-) HOKEN KAGAKU KENKYUSHO
                                                                                                                                                   24-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 cgattaagtgca 375
The present sequence encodes a protein fragment of cytochrome P4501Id6
                           Claim 3; Fig
                                                 Amino acid sequence for liver/kidney microsome (LKM) l antibody human auto-immuno-hepatitis (AIH) type II and hepatitis C
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/transl_except= (pos:#16..318,aa:Xaa)
/note= "Xaa is unspecified"
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/*tag--a
                           9pp; Japanese
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Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which is recognised by AiH Type IIa/IIb LKM1 antibody. The antigens and their complementing antibodies are used in the detection of auto-immuno-hepatitis type II and hepatitis \mathbb C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cytochrome P450; amplification; PCR; yeast NADPH-P450 reductase; safety; fusion carcinogen; mutagen; liver metabolism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ87729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ87729 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human auxillary cytochrome
The nucleotide sequence of the cDNA coding region for the human auxillary cytochrome P450 species 2C6. The 90 to encodes a profit 1497 auxillary cytochrome P450 species 2C6. The 90 to encodes a profit 153-6. amino acids. The cDNA was amplified by PCR using the primers AQ87/63-6. The product was cloned into the yeast expression of the cytochrome P450 to produce the vectors P2D6 for the expression of the cytochrome P450 alone or p2D6R for co-expression with the yeast NADPH-P450 reductase. The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical two protein or in cell extracts, and yeast NADPH-P450 reductase, either as a fused variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused variants (AAQ8718-32), and yeast NADPH-P450 reductase, either as a fused variants (AAQ8718-32), and yeast NADPH-P450 reductase, either as a fused variants (AAQ8718-32), and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for
                                                                                                                                                                                                                                                        Evaluation expressing
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30-JUL-1993;
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Yabusaki Y;
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                                                                                                                                                                                                                         Examples; Page
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                                                                                                                                                                                                                                                             human
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                                                                                                                                                                                                                                                          safety of a chemical cpd. - using recombinant yeast
man cytochrome p450 and a yeast NADPH-P450 reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                 93JP-0180246.
93JP-0201120.
93JP-0208279.
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Matches 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1494
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                                                                                                                                                                                                                                                                                                                                            Human cytochrome P450; amplification; PCK; yeast NADPH-P450 reductase; safety; fusion carcinogen; mutagen; liver metabolism; ds.
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Yabusaki Y;
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                                                                                                                                                                                                20-JUL-1943;
                                                                   Examples; Page 87-89; 124pp; English
                                                                                   expressing
                                                                                             Evaluation
                                                                                                             P-PSDB;
                                                                                                                     WPI; 1995-116991/16
                                                                                                                                                              (HAYA/) HAYASHI K.
(SUMO ) SUMITOMO CHEM CO LTD.
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52; Conserv
                                                                                   of satety of a chemical cpd.
human cytochrome p450 and a
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886
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                                                                                      yeast NADPH-P450
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The nucleotide sequence of the CDNA coding region for the human auxillary cytochrome P450 species 2D6 variant 1. The gene contains a change at base 886 from T to C as compared to the wild type sequence (AAQ87729). This changes the amino acid residue 296 from Cys to Arg. The CDNA was amplified by PCR using the primers AAQ87763-6. The product was cloned into the yeast expression vectors pAAH5N or pAHRR to produce the vectors p2D6 variant 1 for the expression of the cytochrome P450 alone

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RESULT 14
AAQ87731
IU AAQ877
XX AAQ877
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hes 52; Conserv
                      WPI; 1995-116991/16.
p-PSDB; AAR72377.
                                                                                                                                                                                                                                                      21-JUL-1993;
20-JUL-1993;
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                                                                                            Hayashi K,
Yabusaki Y;
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                                                                                                                                                                                   (HAYA/) HAYASHI K.
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93JP-0208279.
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acid from Thr
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Pred. No. 3;
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sm; ds.
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protein; metabolite;
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The nucleotide sequence of the cDNA coding region for the human CC auxillary cytochrome P450 species 2D6 variant 2. The gene contains CC variations at bases 886: Th to C and 1457: C to G as compared to the wild CC type sequence (AAQ87729). These change the amino acid residues 296: Cys CC type sequence (AAQ87729). These change the amino acid residues the CC variation of the cytochrome parameters AAQ87763-6. The product was cloned into the yeast expression CC vectors paalisN or palkR to produce the vectors p2D6 variant 2 for the CC expression of the cytochrome p450 alone or p2D6R variant 2 for CC expression with the yeast NADPH-P450 reductase.

CC co-expression with the yeast NADPH-P450 reductase.

CC compound by reacting the chemical compound with recombinantly produced CC compound by reacting the chemical compound with recombinantly produced CC 2E1 (AAQ87716), or 3A4 (AAQ87717) or their auxillary species and CC variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused CC variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused CC converted into a carcinogenic or mutagenic form through metabolite to CC converted into a carcinogenic or mutagenic form through metabolism in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase
Sequence
     1494 BP;
       248
       A; 508 C;
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Pred. Score

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AAQ87732
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        21-JUL-1993;
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30-JUL-1993;
                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                        Homo
                                                                                                                                                                Human cytochrome P450; amplification yeast NADPH-P450 reductase; safety;
                                                                                                                                                                                       Human auxillary cytochrome P450 species 2D6 variant 3 coding region.
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                                                                                                                                                                                                                                                                                                  405
                                                                                                                                                        carcinogen;
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mes 52; Conserv
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nilarity 61.9%;
Conservative
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         93JP-0180246.
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93JP-0208279.
                                         94EP-0111298
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1457
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                                                                                                                                                                           p450; amplification; PCR;
                                                                                                                                                          liver metabolism;
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"C to G change in variant 1 changes amino
acid from Thr to Ser"
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protein; metabolite;
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The nucleotide sequence of the cDNA coding region for the human CC auxillary cytochrome P450 species 2D6 variant 3. The gene contains a CC change at base 1457 from C to G as compared to the wild type sequence CC (AAQ87729). This changes the amino acid residue 296 from Thr to Ser. The CC cDNA was amplified by PCR using the primers AAQ87763-6. The product was compared to the yeast expression vectors pAAH5N or pAHRR to produce the vectors p2D6 v. riant 3 for the expression of the cyto.hrome P450 alone or p2D6R variant 3 for co-expression with the yeast NADPH-P450 cor p2D6R variant 3 for co-expression with the yeast NADPH-P450 cor p2D6R variant 3 for co-expression with the yeast NADPH-P450 cor p2D6R variant 3 for co-expression with the yeast NADPH-P450 cor p2D6R variant 3 for co-expression with the yeast NADPH-P450 cor p2D6R variant 3 for co-expression with the yeast NADPH-P450 compound with recombinantly core converted human cytochrome P450 molecular species 12 (AAQ87714), 2C9 coround the passion of the chemical compound with recombinantly coround variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a coround variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a coround variant of the chemical compound. The method is useful for the determining whether the chemical compound, or its metaboli will be converted into a carcinogenic or mutagenic form through metabolism in the
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Search completed: March 4, 2002, 05:24:09 Job time: 17678 sec
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P-PSDB; AAR72378.
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Yabusaki Y;
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(SUMO ) SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1494 BP; 248 A; 507 C; 447 G; 292 T; 0 other;
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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US-08-36-05-352-81
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PCT-US96-06583-81
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NAME/KEY: CDS
LOCATION: 49:.717
OTHER INFORMATION:
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                                                                                                                        TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jay, Scott D
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
APPLICANT: Campbell, Kevin P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
MUMBER OF SEQUENCES: B
CORRESPONDENCE ADDRESSE: Hrown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                         FEATURE:
                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                             STATE: C
COUNTRY:
ZIP: 921
                                                                                                                                                                              NAME: Seidman, Stephante L. REGISTRATION NUMBER: $3,779
REFERENCE/DOCKET NUMBER: 54898
                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 07-NOV-1994
CLASSIFICATION: 445
                                                                                                                                                                                                                                                                                                                                                             STREET: 1660 Un
CITY: San Diego
                                                                              TOPOLOGY:
                                                                                                   TYPE: nucleic acid
                                                                                                                                                          TELEPHONE:
                                                                                         STRANDEDNESS:
                                                                                                              LENGTH:
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                                                                                                               1171 base pairs
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             /product= "Gamma subunit of animal
calcium channel"
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US-08-145-658D-22
US-08-145-658D-21
US-09-115-446-1
US-09-115-446-5
US-09-115-446-5
US-08-899-595-4
US-08-899-595-9
US-08-301-162-9
US-08-301-162-9
US-08-424-268-7
US-08-424-268-7
US-08-424-268-7
US-08-424-268-169A-6
US-08-98-42-68-169A-6
US-08-424-268-19
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US-08-1983-10442-19
US-08-1883-10442-19
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22. Appl
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Query Match

6.78;

Score 33.8;

ВВ

Length 1171;

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; APPLICANT: JAY, SCOTT D.;ELLIS, STEVEN B.;HARPOLD, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 11, Application US/08123161A ; Patent No. 5449616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-123-161A-11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: HIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURKENT APPLICATION DATA:
                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN ASSOCIATED TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, Richard D. APPLICANT: Ibrashimov, Oxana B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Campbell, Kevin P. APPLICANT: Roberds, Steven L.
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ibraghimov
APPLICANT: Yang, Bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 GCAGCCGCCATGTCCCCGGACGGAAGCCCCAAAGGTCCGCCTGACCCCTCTTCTGCATCCTG 99
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 qaaqaaqggactqaaccaaccaaqagggclccaaqalcctcqtqaaccalctcctqcalccctg 367
ATTORNEY/AGENT INFORMATION
                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                        STREET: P.O. BOX
CITY: York Harbor
STATE: ME
                                                              FILING DATE: 16
CLASSIFICATION:
                                                                                                                                                                                                                        ZIP: 03911
                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                         ADDRESSEE: Kevin M. Farrell, P.C. STREET: P.O. Rox 999
            APPLICATION NUMBER: 07/946,234 FILING DATE: 14-SEP-92
                                                                                                APPLICATION NUMBER: US/08/123, 161A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56; Conservative
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                                                                                 16-SEP-93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kevin P.
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US-08-483-278-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FATTELL, KEVIN M.
REGISTRATION NUMBER: 35,505
REFERENCE, POCKET NUMBER: UIKF
TELECOMMUNICATION INFORMATION:
TELEPIONE: (207) 363-0528
TELEPAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.5%;
Best Local Similarity 58.9%;
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11
Patent No. !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT:
             TELEFAX: (207) 363-05 INFORMATION FOR SEQ ID NO:
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                                                       FILING DATE: 16-SEP-93
AUTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 45,505
REFERENCE/DOCKET NUMBER: UIKE89-11A5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Campbell, Kevin P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          934 СТСАТСПОСТСКОСССССКАКОСАКОСТСАКОКО 968
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                        STATE: ME
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC 1005/MS 1008
SOFTWARE: Patenth: Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                           APPLICATION NUMBER: 08/123,161
                                                                                                                                                                                                                               APPLICATION NUMBER:
                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                 115313
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AVENTION: NECLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ervasti, James M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Kevin M. Farrell, P.C
                                                (207) 363-0558
        7) 30.
363-0528
- NO: 11:
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Best Local Similarity
Matches 56; Conserve
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US-08-483-278-11
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                                   US-08-910-864-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                         INFORMATION FOR SEA ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1434 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHOD FOR SPECIFICALLY AMPLIFYING A COMA OF AN EXTREMELY TITLE OF INVENTION: SMALL QUANTITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SAKAMOTO, AIJI
APPLICANT: HANAOKA, FUMIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     874 CTGCTCACCCTCCTGCTGCTGCTGCTGCTGCTGCTTCTCACCCTTGCTGCTGCTGGCTAT 933
                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 21650
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: HATLE, LISA A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                  FEATURE:
                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DUS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                NAME/KEY:
                                                                                                                              STRANDEDNESS: double
                                                                                                                                                                                                                     TELEPHONE:
                                                     LOCATION:
                                                                                                                 TOPOLOGY:
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                                                                                                                 linear
                                                     44..1204
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13-AUG-1997
                                                                                                                                                                                                                                                                                                                UMBER: JP 216506/1996
16-AUG-1996
                                                                                                  CINA to IIIRNA
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                                                                                                                                                                                                                                                         07898/017001
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DES 4;
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 Length 1446;
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Query Match

6.5%; Score 12.6;

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5482709-5/c
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; TITLE OF INVENTION: EINERIA ANTIGENIC COMPOSITION WHICH
;ELICITS ANTIHODIES AGAINST AVIAN COCCIDIOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPILICANT: JACOBSON, JAMES W.:STRAUSBERG, ROBERT L.:WILSON, ;SUSAN D.:POPE, SHARON H.:STRAUSBERG, SUSAN L.:RUFF, MICHAEL D.:
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                                                                                                                                                                                                                                                                                                                               5273901-6/c
;Patent No. 5273901
                                                                                                                                                                                                                                                                         APPLICANT: JACOBSON, JAMES W.:STRAUSHERG, KOBERT L.:WILSON, SUSAN D.:POPE, SHARON H.:SFRAUSHERG, SUSAN L.:RUFF,MICHAEL D.:PAUGUSTINE, PATRICIA C.:TANFORTE, HARRY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:5:
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5273901-6
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NUMBER OF SEQUENCES: 11
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                               SEQ ID NO:6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 581,693
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                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              974 GTCATGTGCTGCCGGCGGGAGAAAGGCTGAAAAAC 1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 746,520 FILING DATE: 19-JUN-1985 APPLICATION NUMBER: 627,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05-JUL-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-SEP-1990
                                                                                                                                                                        APPLICATION NUMBER: US/
FILING DAFE: 12-SEP-1990
                                                             APPLICATION NUMBER: 746,520 FILING DATE: 19-JUN-1985 APPLICATION NUMBER: 627,811
                                                                                                                 APPLICATION NUMBER: 215,162
FILING DATE: 05-JHL-1988
                                                FILING DATE:
                LENGTH: 54 4
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ilarity 56.1%;
Conservative
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Pred. No. 0.65;
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Best Local Similarity
Ouery Match
Best Local Similarity 60.3
Whitches 51: Conservative
                                                                                  ORGANISM:
- 08 - 145 - 6581>- 23
                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 18-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 18-JUL-1991
ATTOKNEY/AGENT INFORMATION:
NAME: Brady, Jr., James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "ENERAL INFORMATION:
                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 04-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wolt, Charles R. APPLICANT: Miles, John S. APPLICANT: Spur, Nigel K. APPLICANT: Gough, Alan C.
                                                                                                                                                                                                                                                                        NAME: Brady, Jr., James W.
REGISTRATION NUMBER: 32.115
REFERENCE/DOCKET NUMBER: E82N0.017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-785-9700
TELEPAX: 202-887-0689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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LENGTH: 1569 base pairs
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PRIOR APPLICATION NUMBER: GB 9001181.8
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                                                                                                                                HYPOTHETICAL: I
                                                                                                                                                               MOLECULE TYPE:
                                                                                                                 ORIGINAL SOURCE:
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OPERATING SYSTEM: PC-108/MS-108
SOFTWARE: Patentin Release #1.0, Version #1.40
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STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                POPOLOGY:
                    6.2%;
Similarity 60.7%;
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                                                                                                   Homo sapiens
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                                                                                                                                                                                Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                 CINA to mRNA
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56.1%;
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      Score 31.2; Di
Pred. No. 1.9;
O; Mismatches
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                                       DH 2; Length 1569;
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          Indels
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            Cups
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: Sequence 81, Application US/08599252
; Patent No. 5705443
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Best Local Similarity 53.3%;
Matches 65; Conservative
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APPLICANT: FEBEK, JOHN N.
APPLICANT: GNITKE, ANDREAS
APPLICANT: KIMMEL, HRUYE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFE, KORER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: FIOPPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOPHWARE: Fatentin Release #1.0, Version #1.30 CURRING APPLICATION DATA:
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Cliy: Washington
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421 GA 422
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TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/INSTRET NUMBER: 29, 959
REFERENCE/INSTRET NUMBER: 9058-0001.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/599,252
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                                                                                                                                                   TYPE: nucleic acid
STRANDEDNISS: sincic
ToPOLOGY: linear
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N: 435
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PCT-US96-06352-81
Sequence 81, Application PC/FUS9606352
GENERAL INFORMATION:
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TITLE OF INVENTION: HEMOCHROMATUSIS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 90 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
FILING DATE: 08-MAY-19
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MEDIUM TYPE: Floppy disk
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                                                             APPLICANT:
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1050 base pairs TYPE: nucleic acid STRANDEDNESS: single
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TELEX: 90-4030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MURASHIGE, KATE H. REGISTRATION NUMBER: 29,959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 887-1500
(202) 887-0763
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                                             PEDER, JOHN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version
                              GNIKKE, ANDREAS
   THOMAS,
                KIMMEL,
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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53.38;
   BRUCE E.
WINSTON J.
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PCT-US96-06352-81
                                                                                                                                                                                                            Sequence 81, Application PC/TUS9606583 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Zoon
CITY: Washington
STATE: DC
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APPLICATION NUMBER: US 0
EILING DATE: 09-FEB-1996
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OPERATING SYSTEM: PRIDES/MS-DUS
SOFTWARE: Patentin Recease #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: MORRISON & FOERSTER
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TITLE OF INVENTION: METHOD TO DIAGNOTIFIE OF INVENTION: HEMOCHROMATOSIS
                                                                  APPLICAVE: DKAYNA, DENNIS F.
APPLICANT: FEDER, JOHN N.
APPLICANT: GNIRKE, ANDEAS
APPLICANT: KIMMEL, BRUCE F.
APPLICANT: THOMAS, MINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDLYARY
TITLE OF INVENTION: HEMOCHROMATOSIS
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                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GCCCAAGGTATTGGTGAGGTTGGCAGTGTGGCGTGGGGGGGTGTGGCCCCTCTCTGCT 360
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20006-1888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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                      ADDRESSEE:
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VENTION: METHOD TO DIAGNOSE HEREDITARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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2000 Pennsylvania Ave. N.W., Suite
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                      MORRISON & FOEKSTER
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Pred. No. 2;
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COMPUTER READABLE FORM:

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STATE: COUNTRY:

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Best Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 9053-0001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-FEB-1996
AUTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,9
CURRENT APPLICATION DATA:
                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                      CORRESPONDENCE ADDRESS: No. 58211020 No. 5821102disk of No. 5821102th America, Inc
                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
                                                                                                                                                                                                                                                            APPLICANT: Boominathan, Karuppan APPLICANT: Sandal, Thomas
                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                       11
421 GA 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 geteaagateelegtyaeeateleetyeateelggateggaldtelaetyeleetigtget 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 PCTCTGGGCTCTGCAGGTCCTGCTGCTGCTTCTACCCCTGCTGCAGAAGAAGATGACAA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC:DOS/MS-INOS
COMPUTER DISC. PC:DOS/MS-INOS
            OPERATING SYSTEM:
SOFTWARE: Fast SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                   COMPUTER:
                                                                  MEDIUM TYPE: Diskette
                                                                                                                     COUNTRY:
                                                                                                                                        STATE:
                                                                                                                                                         CITY:
                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 887-0763
TELEX: 90-4030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                      New York
                                                                                                     10174
                                                                                                                                                                    405 Lexington Avenue
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              FastSEQ for Windows Version 2.0
                                            IBM Compatible
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Best Local Similarity 56.4%;
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/OB14565BD Patent No. 5981174
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: HAM PC compatible
OPERATING SYSTEM: PC-bas/MS bas
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               TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-785-9700
                                                                                                       FILING DATE: 18-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/732,223
                                                                                                                                                                                                   APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GEN FIG ASSAY NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Miles, John S. APPLICANT: Spiri, Nigel K. APPLICANT: Gough, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wolf, Charles R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Genomic DNA
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REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 460
                                                   REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: E8280.017
                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2101 L S
CITY: Washington
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                               FILING DATE: 04-NOV 1993
                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
             TELEPHONE:
                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE
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                                                                                     Brady, Jr., James W
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2012-887-0689
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TOPOLOGY: linear
MOLECULE TYPE: CDN
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-145-658D-24
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US-08-145-658D-13
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SEQUENCE CHARACTERISTICS:
LENGTH: 1501 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wolf, Charles R.
APPLICANT: Miles, John S.
APPLICANT: Spurr, Nigel K.
APPLICANT: Gough, Alan C.
TITLE OF INVENTION: GENETIC ASSAY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE AIDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                             TELEFAX: 202-887-0689
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2104
CITY: Washington
STATE: DC
STATE: DC
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MEDIUM TYPE: Floppy disk
TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: GB 9001181.8
APPLICATION NUMBER: GB 9001181.8
FILING DATE: 18-JAN-1990
PRIOR APPLICATION NUMBER: US 07/732,224
APPLICATION NUMBER: US 07/732,224
FILING DATE: 18-JUL-1991
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                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1566 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Brady, Jr., James W.
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: E8280.017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-785-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
FILING DATE: 04-NO
CLASSIFICATION: 43
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2101 L Street N.W.
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                     CDNA to mRNA
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; ANTI-SENSE: NO ; ORIGINAL SOUNCE: ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGAN
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